

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 28, 2006, 13:51:05 ; Search time 188 Seconds
(Without alignments)
911.477 Million cell updates/sec

Title: US-10-616-088-2

Perfect score: 1 MEDTNTITVLSLSTRVTLAF.....KIFCIKQPLPSQHSRVS 390

Sequence: 2024

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

- A_Geneseq_21.*
1: geneseqp19808.*
2: geneseqp19908.*
3: geneseqp20008.*
4: geneseqp20018.*
5: geneseqp20028.*
6: geneseqp20038.*
7: geneseqp20048.*
8: geneseqp20058.*
9: geneseqp20068.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2024	100.0	390	3 AAB02831	AAB02831 Human G p
2	2024	100.0	390	3 AAY71297	AAY71297 Human G p
3	2024	100.0	390	3 AAB62445	AAB62445 Human GPC
4	2024	100.0	390	4 AAB64477	AAB64477 Human G p
5	2024	100.0	390	4 AAB73622	AAB73622 Human G p
6	2024	100.0	390	5 AAM53050	AAM53050 Human G p
7	2024	100.0	390	5 AAB98629	AAB98629 Human G p
8	2024	100.0	390	5 AAB78276	AAB78276 Human G p
9	2024	100.0	390	5 AAM50564	AAM50564 Human G p
10	2024	100.0	390	5 AAG66023	AAG66023 Human G p
11	2024	100.0	390	5 AAB71960	AAB71960 Human G p
12	2024	100.0	390	6 AAB02831	AAB02831 Human G p
13	2024	100.0	390	6 AAB02831	AAB02831 Human G p
14	2024	100.0	390	6 AAB02831	AAB02831 Human G p
15	2024	100.0	390	6 AAB02831	AAB02831 Human G p
16	2024	100.0	390	7 AAB02831	AAB02831 Human G p
17	2024	100.0	390	7 AAB02831	AAB02831 Human G p
18	2024	100.0	390	8 AAB02831	AAB02831 Human G p
19	2024	100.0	390	8 AAB02831	AAB02831 Human G p
20	2024	100.0	390	8 AAB02831	AAB02831 Human G p
21	2024	100.0	390	8 AAB02831	AAB02831 Human G p
22	2024	100.0	390	8 AAB02831	AAB02831 Human G p
23	2024	100.0	390	8 AAB02831	AAB02831 Human G p
24	2024	100.0	390	9 AAB02831	AAB02831 Human G p

25	2024	100.0	391	5 AAM53052	AAM53052 Human G p
26	2024	100.0	392	5 AAM53053	AAM53053 Human G p
27	2019	99.8	390	8 AAB02831	AAB02831 Human G p
28	2008	99.2	390	4 AAM51410	AAM51410 Human GPR
29	2008	99.2	390	6 AAB36416	AAB36416 Human H4
30	1815.5	89.7	357	6 AAB36415	AAB36415 Human H4
31	1671	82.6	336	6 AAB36414	AAB36414 Human H4
32	1433.5	70.8	649	5 AAB02831	AAB02831 Ligand up
33	1413.5	69.8	391	5 AAM50566	AAM50566 Rat hista
34	1377.5	68.1	391	5 AAM50565	AAM50565 Mouse his
35	1377.5	68.1	391	8 ADO29497	ADO29497 Mouse GPC
36	1318.5	65.1	389	5 AAM50567	AAM50567 Guinea pi
37	772	38.1	441	5 AAB23411	AAB23411 Human G-p
38	730	36.1	415	7 AAO29530	AAO29530 Human H3
39	730	36.1	445	6 ABR43668	ABR43668 Monkey hi
40	730	36.1	445	6 ABR57426	ABR57426 Monkey hi
41	730	36.1	445	8 ADP76111	ADP76111 Monkey H3
42	729	36.0	445	2 AAY06323	AAY06323 Rat G pro
43	729	36.0	445	2 AAG67831	AAG67831 Rat musca
44	729	36.0	445	3 AAB15382	AAB15382 Rat G-pro
45	729	36.0	445	6 ABR43669	ABR43669 Rat hista

ALIGNMENTS

RESULT 1	
AA02831	AA02831 standard; protein; 390 AA.
XX	
AC	AA02831;
XX	
DT	22-AUG-2000 (first entry)
DE	
XX	Human G protein coupled receptor hRUP7 protein SEQ ID NO:14.
XX	Human; G protein coupled receptor; GPCR; transmembrane receptor;
KW	identification; agonist; screening; therapeutic; pharmaceutical; mutant.
XX	
OS	Homo sapiens.
XX	
PN	MO200022131-A2.
XX	
PD	20-APR-2000.
XX	
PF	13-OCT-1999; 99WO-US024065.
XX	
PR	13-OCT-1998; 98US-01170496.
PR	12-NOV-1998; 98US-01060297.
PR	20-NOV-1998; 98US-0109213P.
PR	27-NOV-1998; 98US-0110060P.
PR	16-FEB-1999; 99US-0120416P.
PR	26-FEB-1999; 99US-0121852P.
PR	12-MAR-1999; 99US-0123944P.
PR	12-MAR-1999; 99US-0123945P.
PR	12-MAR-1999; 99US-0123946P.
PR	12-MAR-1999; 99US-0123948P.
PR	12-MAR-1999; 99US-0123949P.
PR	12-MAR-1999; 99US-0123951P.
PR	12-MAR-1999; 99US-0123951P.
PR	28-MAY-1999; 99US-0136437P.
PR	28-MAY-1999; 99US-0136437P.
PR	28-MAY-1999; 99US-0136439P.
PR	28-MAY-1999; 99US-0137127P.
PR	28-MAY-1999; 99US-0137131P.
PR	28-MAY-1999; 99US-0137567P.
PR	29-JUN-1999; 99US-0141448P.
PR	27-AUG-1999; 99US-0151114P.
PR	03-SEP-1999; 99US-0152524P.
PR	29-SEP-1999; 99US-0156555P.
PR	29-SEP-1999; 99US-0156633P.
PR	29-SEP-1999; 99US-0156634P.
PR	29-SEP-1999; 99US-0156653P.
PR	01-OCT-1999; 99US-0157280P.

PR 01-OCT-1999; 99US-0157281P.
 PR 01-OCT-1999; 99US-0157282P.
 PR 01-OCT-1999; 99US-0157293P.
 PR 01-OCT-1999; 99US-0157294P.
 PR 12-OCT-1999; 99US-00416760.
 PR 12-OCT-1999; 99US-00417044.
 (AREN-) ARENA PHARM INC.
 Behan DP, Lehmann-Brutsmma K, Chalmers DT, Chen R, Dang HT,
 Gore M, Liaw CW, Lin I, Lowitz K, White C;
 WPI; 2000-317986/27.
 N-PSDB; AAA46023.
 Non-endogenous, human G protein-coupled receptors for screening receptor,
 inverse or partial agonists useful as therapeutic agents.
 Example 1; Page 89-90; 187pp; English.
 The present invention describes transmembrane receptors, preferably human
 G protein coupled receptors (GPCR), for which the endogenous ligand is
 unknown (orphan GPCR receptors). More specifically the present invention
 relates to non-endogenous, constitutively activated versions of a human
 GPCR. These non-endogenous human GPCRs can be useful for the direct
 identification of candidate compounds as receptor agonists, inverse
 agonists or partial agonists for use as pharmaceutical agents. AAA46017
 to AAA46126 and AAB02825 to AAB02859 represent sequences used in the
 exemplification of the present invention
 Sequence 390 AA;
 Query Match 100.0%; Score 2024; DB 3; Length 390;
 Best Local Similarity 100.0%; Pred. No. 1.5e-211;
 Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPDNTSTINISLSTRVTLAFPMSLVAFIMGNALVILAFVVDKXLRHRSYFFLNLAIS 60
 DB 1 MPDNTSTINISLSTRVTLAFPMSLVAFIMGNALVILAFVVDKXLRHRSYFFLNLAIS 60
 QY 61 DFFGVGISIPYIPIHTLFEMDFGKEICVFMITDYLCTASVNIIVISYRYISVSNAY 120
 DB 61 DFFGVGISIPYIPIHTLFEMDFGKEICVFMITDYLCTASVNIIVISYRYISVSNAY 120
 QY 121 SYRTOHTGVLTIVLMAVAVTLAVLNGPMILVSESWKDESGCEPGFSEMYLAIITSF 180
 DB 121 SYRTOHTGVLTIVLMAVAVTLAVLNGPMILVSESWKDESGCEPGFSEMYLAIITSF 180
 QY 181 LEFVTPITLVAFFMNTIYSLMKRDHLSCQSHGCLTVSSNICGHSRGLSSRRSLISA 240
 DB 181 LEFVTPITLVAFFMNTIYSLMKRDHLSCQSHGCLTVSSNICGHSRGLSSRRSLISA 240
 QY 241 STEVPASFHSRRORRKSLSMFSSTKKNSTIASKMGFSQSDSYALHQRHVELLPARR 300
 DB 241 STEVPASFHSRRORRKSLSMFSSTKKNSTIASKMGFSQSDSYALHQRHVELLPARR 300
 QY 301 LAKSLALILGVAFACWAPYSILFTIVLSFYSSATGPKSVYRIAFWLQWENSFVNPLLYPL 360
 DB 301 LAKSLALILGVAFACWAPYSILFTIVLSFYSSATGPKSVYRIAFWLQWENSFVNPLLYPL 360
 QY 361 CHKRFOKAFLKIFCIKKQPLPSOHSRSVSS 390
 DB 361 CHKRFOKAFLKIFCIKKQPLPSOHSRSVSS 390
 RESULT 2
 AA71297 ID AA71297 standard; protein; 390 AA.
 AA71297;
 02-NOV-2000 (first entry)

DE Human orphan G protein-coupled receptor hrUP7.
 XX Human, orphan G protein-coupled receptor; GPCR; hrUP7; drug screening;
 KW transmembrane receptor; signal cascade.
 XX Homo sapiens.
 OS
 XX W0200031258-A2.
 PN
 XX
 PD 02-JUN-2000.
 XX
 PF 13-OCT-1999; 99MO-US023687.
 XX
 PR 20-NOV-1998; 98US-0109213P.
 PR 16-FEB-1999; 99US-0120416P.
 PR 26-FEB-1999; 99US-0121852P.
 PR 12-MAR-1999; 99US-0123946P.
 PR 12-MAR-1999; 99US-0123949P.
 PR 28-MAY-1999; 99US-0136436P.
 PR 28-MAY-1999; 99US-0136437P.
 PR 28-MAY-1999; 99US-0136439P.
 PR 28-MAY-1999; 99US-0136567P.
 PR 28-MAY-1999; 99US-0137127P.
 PR 28-MAY-1999; 99US-0137131P.
 PR 29-JUN-1999; 99US-0141448P.
 PR 29-SEP-1999; 99US-0156555P.
 PR 29-SEP-1999; 99US-0156633P.
 PR 29-SEP-1999; 99US-0156634P.
 PR 29-SEP-1999; 99US-0156633P.
 PR 01-OCT-1999; 99US-0157280P.
 PR 01-OCT-1999; 99US-0157281P.
 PR 01-OCT-1999; 99US-0157282P.
 PR 01-OCT-1999; 99US-0157293P.
 PR 01-OCT-1999; 99US-0157294P.
 PR 12-OCT-1999; 99US-00416760.
 PR 12-OCT-1999; 99US-00417044.
 (AREN-) ARENA PHARM INC.
 Chen R, Dang HT, Liaw CW, Lin I;
 WPI; 2000-400068/34.
 N-PSDB; AAD01124.
 Novel human orphan G protein-coupled receptors and the encoding cDNAs for
 use in the identification of G protein-coupled receptor agonists.
 Claim 26; Page 60-61; 102pp; English.
 The present amino acid sequence is the hrUP7, an endogenous human orphan
 G protein-coupled receptor (GPCR). The full length hrUP7 cDNA was cloned
 by RT-PCR using human peripheral leucocyte cDNA as template. The orphan
 GPCR of the invention, like all GPCRs has seven transmembrane alpha
 helices with an extracellular N-terminus and an intracellular C-terminus.
 However, no endogenous ligands has yet been identified for the proteins
 of the invention. The orphan GPCRs may be used in the identification of
 their endogenous ligands, and to screen potential GPCR agonists and
 antagonists for use as pharmaceutical agents. The proteins may also be
 used in the study of GPCR-mediated signalling cascades, and to elucidate
 their precise role in normal and diseased human conditions. Nucleic acid
 encoding human orphan GPCRs may be used for tissue localisation
 expression analysis to provide information about their function in
 healthy and pathological states
 Sequence 390 AA;
 Query Match 100.0%; Score 2024; DB 3; Length 390;
 Best Local Similarity 100.0%; Pred. No. 1.5e-211;
 Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPDNTSTINISLSTRVTLAFPMSLVAFIMGNALVILAFVVDKXLRHRSYFFLNLAIS 60
 DB 1 MPDNTSTINISLSTRVTLAFPMSLVAFIMGNALVILAFVVDKXLRHRSYFFLNLAIS 60

QY	61	DEPVGVISLPIPLIIPHTLPEMDPCKEICVFWLTLDYLLCTASVYNIYLISYDRILSVENAV	120
QY	61	DEPVGVISLPIPLIIPHTLPEMDPCKEICVFWLTLDYLLCTASVYNIYLISYDRILSVENAV <td>120</td>	120
Db	61	DEPVGVISLPIPLIIPHTLPEMDPCKEICVFWLTLDYLLCTASVYNIYLISYDRILSVENAV <td>120</td>	120
QY	121	SVRTGHTGVKILVTLMVAWVIAFLVNGPMIIVSESKMGESCEPCGFSEWYILATISF <td>180</td>	180
Db	121	SVRTGHTGVKILVTLMVAWVIAFLVNGPMIIVSESKMGESCEPCGFSEWYILATISF <td>180</td>	180
QY	181	LEFVLPIVLIIVAEFNNNIYMSLWKRDLISRCQSHPGILTAVSNICGHSFRRLSSRRLSA <td>240</td>	240
Db	181	LEFVLPIVLIIVAEFNNNIYMSLWKRDLISRCQSHPGILTAVSNICGHSFRRLSSRRLSA <td>240</td>	240
QY	241	STEVVASFHSERQRRKSSLMFSRTGMNSVTIASKMGSPFQSPSVALLHOREHYELLRAR <td>300</td>	300
Db	241	STEVVASFHSERQRRKSSLMFSRTGMNSVTIASKMGSPFQSPSVALLHOREHYELLRAR <td>300</td>	300
QY	301	LAKSLAILLGVAVCAWAPYSLFTIYLSFYSSATGPKRSWYRIAFWLQWENSFVNPLLYPL <td>360</td>	360
Db	301	LAKSLAILLGVAVCAWAPYSLFTIYLSFYSSATGPKRSWYRIAFWLQWENSFVNPLLYPL <td>360</td>	360
QY	361	CHKRFQKAPLKIFCIKKQPLPSGHSRSVSS <td>390</td>	390
Db	361	CHKRFQKAPLKIFCIKKQPLPSGHSRSVSS <td>390</td>	390
RESULT 3			
AAB62445			
ID	AAB62445	standard; protein, 390 AA.	
XX			
AC	AAB62445;		
XX			
DT	09-JUL-2001	(first entry)	
XX			
DE	Human GPCR-like polypeptide, PFI-013.		
XX			
KW	G-protein coupled receptor; GPCR; PFI-013; anti-allergic; antiasthmatic;		
KM	antiinflammatory; vasotrophic; antidiabetic; anorectic; cytostatic; human;		
KM	osteopathic; neuroprotective; nootropic; dermatological; gynecological;		
KW	signal transduction.		
XX			
OS	Homo sapiens.		
XX			
PN	EPI096009-A1.		
XX			
PD	02-MAY-2001.		
XX			
XX	24-OCT-2000; 2000EP-00309364.		
XX			
PR	29-OCT-1999; 99GB-00025641.		
PR	20-APR-2000; 2000GB-00009973.		
XX			
PA	(PFI2) PRIZER LTD.		
PA	(PFI2) PRIZER INC.		
XX			
P1	Peter B, O'reilly MA;		
XX			
DR	WPI; 2001-309854/33.		
XX			
XX	N-PSDB; AAF83203.		
PT	New G-protein coupled receptor-like polypeptide, polynucleotide for		
PT	screening drug candidates for treating diseases associated with signal		
PT	transduction e.g. allergic, inflammatory, pulmonary, neoplastic diseases.		
XX			
XX	Claim 22; Page 44; 66pp; English.		
CC	This is a human G-protein coupled receptor (GPCR)-like polypeptide, PFI-		
CC	013, encoded by cDNA of NCIMB 41073. The PFI-013 protein can be expressed		
CC	by standard recombinant methodology. Antibodies and modulators of PFI-013		
CC	are useful in the manufacture of a medicament for treating allergic		
CC	disorder, including extrinsic asthma, immunological disorders, such as		
CC	intrinsic asthma, vasculitic granulomatous disease, interstitial and		
CC	other pulmonary disease, including chronic obstructive pulmonary disease		

Query Match	Best Local Similarity	Score	DB 4	Length	390
Matches	390	Conservative	0	Mismatches	0
				Indels	0
				Gaps	0
Sequence 390 AA:					
1	MDPNSTINISLSTRVTLAFPMGSLVAFALMGNALVTLAPVDKDLRHRSYFFLNLAI	60			
2	1	MDPNSTINISLSTRVTLAFPMGSLVAFALMGNALVTLAPVDKDLRHRSYFFLNLAI	60		
3	61	DFEFGVISIPLYIPHTLFEMDFGEICVFMLTDTYLICTASVNIIVLISYRYSVSNAY	120		
4	61	DFEFGVISIPLYIPHTLFEMDFGEICVFMLTDTYLICTASVNIIVLISYRYSVSNAY	120		
5	121	SYRTOHGVGLKIYTLMAVAVWLAFVANGPMILVSESWKDESGECPGFSEMYILATISF	180		
6	121	SYRTOHGVGLKIYTLMAVAVWLAFVANGPMILVSESWKDESGECPGFSEMYILATISF	180		
7	181	LEFYIPVILVAFPMNIYMSLWKRDHLSCQSHPEGLTAVSSNTICGSPFGRGLSSRRSLSA	240		
8	181	LEFYIPVILVAFPMNIYMSLWKRDHLSCQSHPEGLTAVSSNTICGSPFGRGLSSRRSLSA	240		
9	241	STEVPASFEHSEORRKSLSMPSSRTKNSNTIASIKMGSEFSSQSDVALHOREHVELLRAR	300		
10	241	STEVPASFEHSEORRKSLSMPSSRTKNSNTIASIKMGSEFSSQSDVALHOREHVELLRAR	300		
11	301	LAKSLATILGVFAVCMAFYSLETTVLSEFYSSATGPKSWMYRIAFMLQMFNSFVNPLLYPL	360		
12	301	LAKSLATILGVFAVCMAFYSLETTVLSEFYSSATGPKSWMYRIAFMLQMFNSFVNPLLYPL	360		
13	361	CHKRFOKAPLKICIKKQPLPSQHSRVS	390		
14	361	CHKRFOKAPLKICIKKQPLPSQHSRVS	390		
15	AAAG64477	standard; protein; 390 AA.			
16	AAAG64477				
17	25-SEP-2001	(first entry)			
18	Human G protein-coupled receptor protein BG26.				
19	Human; G protein-coupled receptor protein BG26; histamine H3; histamine; altering intracellular cAMP concentration; regulating signal transduction.				
20	Homo sapiens.				
21	WO200146414-A1.				
22	28-JUN-2001.				
23	20-DEC-2000; 2000WO-JP009038.				
24	20-DEC-1999; 99JP-00361687.				

(BANY) BANYU PHARM CO LTD.
 XX Itcadani H, Nakamura T, Tanaka K, Ohta M,
 XX WPI, 2001-441675/47.
 DR N-PSDB; AAH47911.
 XX
 PT G protein-coupled receptor protein BG26, with activity of binding to
 PT histamine and capable of changing intracellular cAMP concentration in
 PT response to its stimulus, applicable as tool in screening ligands or drug
 PT candidates.
 XX
 XX Claim 1, Page 41-44; 50pp; Japanese.
 CC The present sequence is that of the human G protein-coupled receptor
 CC protein BG26, which shows significant homology with histamine H3, with
 CC activity of binding to histamine and capable of changing intracellular
 CC cAMP concentration in response to its stimulus. The protein is applicable
 CC as a tool in screening ligands or drug candidates for regulating signal
 CC transduction from such protein and treating diseases associated with its
 CC abnormality
 CC
 XX Sequence 390 AA;
 SO
 Query Match 100.0%; Score 2024; DB 4; Length 390;
 Best Local Similarity 100.0%; Pred. No. 1.5e-211;
 Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPDNTNINISLSTRVTLAFPMISLAFMIGNALVILAFVDDKNLRHRSYFPLNLAIS 60
 DB 1 MPDNTNINISLSTRVTLAFPMISLAFMIGNALVILAFVDDKNLRHRSYFPLNLAIS 60
 QY 61 DFEVGVISIPLYIPHTLFEMDFGKEICVFWLTDTYLLCTASVYNIILSYDRYLSVSNV 120
 DB 61 DFEVGVISIPLYIPHTLFEMDFGKEICVFWLTDTYLLCTASVYNIILSYDRYLSVSNV 120
 QY 121 SYRQHGQVLTQYTLMAVAVLAVNGPMLVSESWDESEEPGFSPWYLLATTSF 180
 DB 121 SYRQHGQVLTQYTLMAVAVLAVNGPMLVSESWDESEEPGFSPWYLLATTSF 180
 QY 181 LEFVTPVILVAFPMNIYMSLMKRDHLSCQSHFGLTAVSNIIGHSFGRSLSSRSISA 240
 DB 181 LEFVTPVILVAFPMNIYMSLMKRDHLSCQSHFGLTAVSNIIGHSFGRSLSSRSISA 240
 QY 241 STEVPASFHSERQRRKSSLMFSSRTKNSNTIASKMSFSQSDVALHQRHVELLRAR 300
 DB 241 STEVPASFHSERQRRKSSLMFSSRTKNSNTIASKMSFSQSDVALHQRHVELLRAR 300
 QY 301 LAKSLAILLGVFANCMAPYSLFTVLSFYSSATGPKSVWYRIATWLMQFNFNPLLYPL 360
 DB 301 LAKSLAILLGVFANCMAPYSLFTVLSFYSSATGPKSVWYRIATWLMQFNFNPLLYPL 360
 QY 361 CCKRFFOKAFKIFCIKOPKOPPSOHSRSYSS 390
 DB 361 CCKRFFOKAFKIFCIKOPKOPPSOHSRSYSS 390
 *
 RESULT 5
 AAB73622
 ID AAB73622 standard; protein, 390 AA.
 XX
 AC AAB73622;
 XX
 DT 10-AUG-2001 (first entry)
 XX
 DE Human G protein-coupled receptor AXOR35.
 XX
 XX AXOR35; human; G protein-coupled receptor; 7TM receptor;
 KM histamine H3 receptor homologue; infection; viral; bacterial; fungal;
 KM protozoan; HIV-1; HIV-2; pain; cancer; diabetes; obesity; anorexia;
 KM bulimia; osteoporosis; asthma; allergy; urinary retention;
 KM acute heart failure; hypotension; hypertension; angina pectoris;
 KM myocardial infarction; stroke; ulcer; migraine; vomiting;
 KM

KW psychotic disorder; neurological disorder; anxiety; schizophrenia;
 KM manic depression; bipolar disorder; depression; delirium; dementia;
 KM severe mental retardation; dyskinesia; Parkinson's disease;
 KM Huntington's disease; Gilles de la Tourette's syndrome; lymphocyte;
 KM macrophage; eosinophil; neutrophil; function modulation;
 KM autoimmune disorder; pulmonary disorder; gene therapy; vaccine;
 KM drug screening; signal transduction; transgenic animal; drug discovery.
 XX
 OS Homo sapiens.
 XX
 PN WO200133221-A1.
 XX
 PD 10-MAY-2001.
 XX
 PF 26-OCT-2000; 2000WO-US029461.
 XX
 PR 02-NOV-1999; 99US-00431898.
 PR 03-FEB-2000; 2000US-00497790.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PI Aubart KM, Bergsma DJ, Fitzgerald LR, Graybill TL, Li X;
 PI Michalovich D, Morrow DM, Zhu Y;
 XX
 DR WPI, 2001-316464/33.
 DR N-PSDB; AAH24007.
 XX
 PT Novel G-protein coupled receptor polypeptide and polynucleotide for
 PT treating cancer, autoimmune, pulmonary, cardiovascular and neurological
 PT disorders and for identifying modulators useful for treating asthma.
 XX
 PS Claim 1, Page 50-51; 54pp; English.
 XX
 CC The invention relates to the human G protein-coupled receptor AXOR35
 CC (AAB73621), to cDNA encoding AXOR35 (AAH24006), and to AXOR35 fragments
 CC and variants. Like all G protein-coupled receptors, AXOR35 has 7 putative
 CC transmembrane domains and is involved in signal transduction. AXOR35 has
 CC homology and structural similarity with G protein-coupled receptors such
 CC as the human histamine H3 receptor. The invention also relates to
 CC expression vectors and host cells comprising AXOR35 DNA, to recombinant
 CC expression of AXOR35, and to an AXOR35-specific antibody. AXOR35 proteins
 CC and nucleotides may be used to treat a wide variety of disorders
 CC including bacterial, fungal, protozoal and viral infections, particularly
 CC HIV-1 or HIV-2 infections; pain; cancers; benign prostatic hypertrophy;
 CC diabetes; obesity; anorexia; bulimia; osteoporosis; asthma; allergies;
 CC urinary retention; acute heart failure; hypotension; hypertension; angina
 CC pectoris; myocardial infarction; stroke; ulcers; migraine; vomiting;
 CC psychotic and neurological disorders such as anxiety, schizophrenia,
 CC manic depression, depression, delirium, dementia, and severe mental
 CC retardation, and dyskinesias, such as Parkinson's disease, Huntington's
 CC disease or Gilles de la Tourette's syndrome. AXOR35 proteins and
 CC nucleotides are useful as vaccines, and AXOR35 proteins, nucleotides and
 CC antibodies may be used in screening compounds for their ability to
 CC modulate AXOR35 activity or expression. Such AXOR35 modulators are
 CC particularly useful for treating asthma, and inhibiting or promoting the
 CC function of lymphocytes, macrophages, eosinophils or neutrophils in
 CC asthmatic lung. AXOR35 proteins, nucleotides and antibodies are also
 CC useful for diagnosing or determining susceptibility of an individual to a
 CC disease via the detection of abnormal levels of protein or mRNA, or via
 CC the detection of mutations in the corresponding gene. AXOR35 proteins are
 CC also useful for inducing an immunological response in a mammal against
 CC the above diseases, and for antibody production. AXOR35 nucleotides are
 CC also useful as diagnostic reagents, in chromosome localisation and tissue
 CC expression studies, and for producing transgenic animals useful in drug
 CC discovery. AXOR35-specific antibodies are useful for purifying the AXOR35
 CC protein or fragments thereof, and are also useful for treating conditions
 CC associated with the expression of the AXOR35 protein. The present
 CC sequence represents human AXOR35
 XX
 SO Sequence 390 AA;
 Query Match 100.0%; Score 2024; DB 4; Length 390;

Best Local Similarity 100.0%; Pred. No. 1.5e-211; Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPDNTNINSLSTRVTLAFPMSLVAFALMGALVILAFVVDKXLRHRSYFFLNLAI 60
 DB 1 MPDNTNINSLSTRVTLAFPMSLVAFALMGALVILAFVVDKXLRHRSYFFLNLAI 60
 QY 61 DFFVGVSIPLYIPIHTLFEMDFGKEICVFWLTTDYLLCTASVYNIYLISDRYLSVSNV 120
 DB 61 DFFVGVSIPLYIPIHTLFEMDFGKEICVFWLTTDYLLCTASVYNIYLISDRYLSVSNV 120
 QY 121 SYRQHTGVLTIVLMAVAVLAFVNGPMILVSESMKDESGECPGFSEWYLLATISF 180
 DB 121 SYRQHTGVLTIVLMAVAVLAFVNGPMILVSESMKDESGECPGFSEWYLLATISF 180
 QY 181 LEFVPIVILVAFNMNIYWSLMKRDHLSCOSHPGLTAVSSNICGHSFRGLSSRSLSA 240
 DB 181 LEFVPIVILVAFNMNIYWSLMKRDHLSCOSHPGLTAVSSNICGHSFRGLSSRSLSA 240
 QY 241 STEVPASFSESRQRKSSLMFSSRTKNSNTIASKMGFSQSDSVALHOREVELLPARR 300
 DB 241 STEVPASFSESRQRKSSLMFSSRTKNSNTIASKMGFSQSDSVALHOREVELLPARR 300
 QY 301 LAKSIALLLGVFAVCMAPYSLEFTVLSFYSSATGPKSVWVRIAFWLMFNSFVNPLLYPL 360
 DB 301 LAKSIALLLGVFAVCMAPYSLEFTVLSFYSSATGPKSVWVRIAFWLMFNSFVNPLLYPL 360
 QY 361 CHKRFOKAFKIFCIKKQPLPSQHSRSVSS 390
 DB 361 CHKRFOKAFKIFCIKKQPLPSQHSRSVSS 390

RESULT 6
 AAMS3050
 ID AAMS3050 standard; protein; 390 AA.
 XX
 XX AAMS3050;
 DT 26-MAR-2002 (first entry)
 XX
 XX Human G protein-coupled receptor nGPCR-2067.

KM Human; nGPCR-2067, G protein-coupled receptor, 7TM receptor;
 KM signal transduction; mental disorder; central nervous system disease;
 KM metabolic disease; infection; HIV-1; HIV-2; pain; neurological disorder;
 KM psychotic disorder; Huntington's disease; schizophrenia; migraine;
 KM depression; anxiety; bipolar disorder; dementia; Alzheimer's disease;
 KM Parkinson's disease; proliferative disorder; cancer; psoriasis;
 KM benign prostatic hypertrophy; diabetes; dyslipidaemia; obesity; anorexia;
 KM thyroid disorder; cardiovascular disease; hypertension; hypertension;
 KM thrombosis; myocardial infarction; cardiomyopathy; atherosclerosis;
 KM inflammatory conditions; autoimmune disorder; rheumatoid arthritis;
 KM hormonal disorder; renal failure; anti-HIV; analgesic; cytostatic;
 KM anti-diabetic; metabolic; hypertensive; hypotensive; thrombolytic;
 KM cardiac; antihypertensive; neuroleptic; antipsychotic;
 KM antiparkinsonian; tranquiliser; antidepressant; neuroprotective;
 KM anticonvulsant; antiinflammatory; antidiabetic; antineumatic; antiarthritic;
 KM antisporadic; gene therapy; receptor.

OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH 19..41
 FT /label= Transmembrane_domain_1
 FT 52..74
 FT /label= Transmembrane_domain_2
 FT 86..110
 FT /label= Transmembrane_domain_3
 FT 128..146
 FT /label= Transmembrane_domain_4
 FT 172..194
 FT /label= Transmembrane_domain_5
 FT 305..326
 FT Domain

FT /label= Transmembrane_domain_6
 FT 342..360
 FT /label= Transmembrane_domain_7
 FT Domain
 XX
 XX MO200185793-A2.
 XX
 XX 15-NOV-2001.
 XX
 XX 08-MAY-2001; 2001MO-US014750.
 XX
 XX 08-MAY-2000; 2000US-0203108P.
 XX
 XX (PHAA) PHARMACIA & UJOHN CO.
 XX
 XX Lind P, Sejlitz T, Vogel G, Wood LS;
 XX
 XX WPI: 2002-062240/08.
 XX
 XX N-PSDB; ABA02496.
 XX
 XX
 XX New polynucleotide, useful for identifying modulator compounds which are
 XX used for treating psoriasis, schizophrenia, diabetes, encodes the novel G
 XX protein-coupled receptor (nGPCR) polypeptide (nGPCR-2067).
 XX
 XX Claim 31; Page 63; 100pp; English.

CC This sequence represents a novel human G protein-coupled receptor (GPCR)
 CC designated nGPCR-2067. Like all GPCRs, nGPCR-2067 has 7 putative
 CC transmembrane domains and is involved in signal transduction. The
 CC invention also relates to expression vectors and host cells comprising
 CC nucleic acids encoding nGPCR-2067, to recombinant expression of nGPCR-
 CC 2067, to antibodies specific for nGPCR-2067, to drug screening methods
 CC that use nGPCR-2067, and to modulators of nGPCR-2067 activity. nGPCR-2067
 CC nucleic acid sequences may be used to isolate nGPCR-2067 allelic variants
 CC and species homologues and may also be used in genetic mapping. The
 CC invention also discloses the use of nGPCR-2067 nucleic acids in screening
 CC for a predisposition to nGPCR-2067-associated hereditary mental
 CC disorders, or for the diagnosis of these disorders. nGPCR-2067 nucleic
 CC acids may additionally be used to generate transgenic animals, including
 CC knockout animals, which may provide an insight into treating a variety of
 CC human disorders, and may also be used in the design of antisense
 CC molecules for suppressing expression of nGPCR-2067 in cells. nGPCR-2067,
 CC and nGPCR-2067 modulators may be used to treat a wide variety of medical
 CC conditions, particularly mental disorders, central nervous system
 CC diseases, and metabolic diseases. Diseases that may be treated include
 CC viral infections, particularly HIV-1 or HIV-2 infections; pain; central
 CC nervous system, neurological and psychotic disorders such as Huntington's
 CC disease, schizophrenia, migraine, depression, anxiety, bipolar disorder,
 CC dementia, Alzheimer's disease, and Parkinson's disease; proliferative
 CC disorders such as cancer, benign prostatic hypertrophy and psoriasis;
 CC metabolic disorders such as diabetes, dyslipidaemia, obesity, and
 CC anorexia; thyroid disorders; cardiovascular diseases such as hypertension,
 CC hypertension, thrombosis, myocardial infarction, cardiomyopathies, and
 CC atherosclerosis; inflammatory conditions; autoimmune disorders (e.g.,
 CC rheumatoid arthritis); hormonal disorders; and renal failure

XX
 XX SQ Sequence 390 AA;
 XX
 XX Query Match 100.0%; Score 2024; DB 5; Length 390;
 XX Best Local Similarity 100.0%; Pred. No. 1.5e-211;
 XX Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPDNTNINSLSTRVTLAFPMSLVAFALMGALVILAFVVDKXLRHRSYFFLNLAI 60
 DB 1 MPDNTNINSLSTRVTLAFPMSLVAFALMGALVILAFVVDKXLRHRSYFFLNLAI 60
 QY 61 DFFVGVSIPLYIPIHTLFEMDFGKEICVFWLTTDYLLCTASVYNIYLISDRYLSVSNV 120
 DB 61 DFFVGVSIPLYIPIHTLFEMDFGKEICVFWLTTDYLLCTASVYNIYLISDRYLSVSNV 120
 QY 121 SYRQHTGVLTIVLMAVAVLAFVNGPMILVSESMKDESGECPGFSEWYLLATISF 180
 DB 121 SYRQHTGVLTIVLMAVAVLAFVNGPMILVSESMKDESGECPGFSEWYLLATISF 180

QY 181 LEFVPIVILVAYFNNMNIYSLMKRDHLSRCQSHPGTLAVSNICGHSFRGLSSRRSLA 240
 DB 181 LEFVPIVILVAYFNNMNIYSLMKRDHLSRCQSHPGTLAVSNICGHSFRGLSSRRSLA 240
 QY 241 STEVPASFSEERQRRKSSLMFSSRTKNSNTIASKMGSFQSDSVALLHOREHVELLARR 300
 DB 241 STEVPASFSEERQRRKSSLMFSSRTKNSNTIASKMGSFQSDSVALLHOREHVELLARR 300
 QY 301 LAKSLAILLGVAFCWAPYSLSFTIVLSFYSSATGPKSVWTRIAFWLQWNSFVNPLLYPL 360
 DB 301 LAKSLAILLGVAFCWAPYSLSFTIVLSFYSSATGPKSVWTRIAFWLQWNSFVNPLLYPL 360
 QY 361 CHKRFOKAPLKIFCIKKOPLPSQHSRSVSS 390
 DB 361 CHKRFOKAPLKIFCIKKOPLPSQHSRSVSS 390

RESULT 7

ABP98629 standard; protein; 390 AA.
 ID ABB98629

AC ABB98629;
 XX
 XX

DT 13-JUN-2003 (first entry)

DE Human histamine receptor SP9144.

XX human; histamine receptor; chromosome 18; anti-inflammatory;
 XX anti-asthmatic; anti-allergic; dermatological; cerebroprotective; stroke;
 KW anti-migraine; cardiac; anti-rheumatic; anti-arthritis; antiporiatic;
 KW neuroprotective; inflammation; asthma; allergy; atopic dermatitis;
 KW myocardial infarction; migraine; chronic obstructive pulmonary disease;
 KW rheumatoid arthritis; multiple sclerosis; inflammatory bowel disease;
 KW psoriasis; receptor.

XX Homo sapiens.

PN US6204017-B1.

PD 20-MAR-2001.

PF 07-OCT-1999; 99US-00414010.

PR 07-OCT-1999; 99US-00414010.

XX (SCHE) SCHERING CORP.

PI Bahan JX, Hedrick JA, Laz TM, Monsma FJ, Morse KL, Umland SP;
 PI Wang S;

XX WPI; 2002-442063/47.

DR N-PSDB; ABZ80663.

XX New nucleic acid encoding antigenic part of human histamine receptor,
 PT useful for preparing antibodies, e.g. for treating-histamine related
 PT disorders.

XX Example 1; Col 27-30; 19pp; English.

XX This sequence represents the amino acid sequence of a human histamine
 CC receptor (HR) designated SP9144. The sequence was isolated by searching
 CC databases with the sequence of known G-coupled protein receptor (GPCR).
 CC The gene is used for recombinant production of HR and for preparing
 CC antibodies (Ab). These Ab are used to purify HR by immunoprecipitation
 CC chromatography, in immunoscreening of histamine receptor, to identify cDNA
 CC clones that express the receptor, as antagonist to block binding of
 CC histamine (for treating any histamine-associated disorder) and to
 CC generate anti-idiotypic antibodies. Agonists and antagonists of the HR
 CC protein can be used in the treatment of e.g. inflammation, asthma,
 CC allergy, atopic dermatitis, stroke, myocardial infarction, migraine,
 CC chronic obstructive pulmonary disease, rheumatoid arthritis, multiple
 CC sclerosis, inflammatory bowel disease and psoriasis

SQ Sequence 390 AA;

Query Match 100.0%; Score 2024; DB 5; Length 390;
 Best Local Similarity 100.0%; Pred. No. 1.5e-211;
 Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPDNTNINLSSTRVTLAFMGLVAFALMGVALVILFVVDKNLRHRSYFFNLAIIS 60
 DB 1 MPDNTNINLSSTRVTLAFMGLVAFALMGVALVILFVVDKNLRHRSYFFNLAIIS 60
 QY 61 DFEVGIISIPLYIPHTLFEMDFGKEICVFWLTTDYLLCTASVYNIYLISDYRLSVSNV 120
 DB 61 DFEVGIISIPLYIPHTLFEMDFGKEICVFWLTTDYLLCTASVYNIYLISDYRLSVSNV 120
 QY 121 SYRTOHTGVLTITLVAAVWVLAFLVNGPMILVSEMDGEGCEGFSEWYILATISF 180
 DB 121 SYRTOHTGVLTITLVAAVWVLAFLVNGPMILVSEMDGEGCEGFSEWYILATISF 180
 QY 181 LEFVPIVILVAYFNNMNIYSLMKRDHLSRCQSHPGTLAVSNICGHSFRGLSSRRSLA 240
 DB 181 LEFVPIVILVAYFNNMNIYSLMKRDHLSRCQSHPGTLAVSNICGHSFRGLSSRRSLA 240
 QY 241 STEVPASFSEERQRRKSSLMFSSRTKNSNTIASKMGSFQSDSVALLHOREHVELLARR 300
 DB 241 STEVPASFSEERQRRKSSLMFSSRTKNSNTIASKMGSFQSDSVALLHOREHVELLARR 300
 QY 301 LAKSLAILLGVAFCWAPYSLSFTIVLSFYSSATGPKSVWTRIAFWLQWNSFVNPLLYPL 360
 DB 301 LAKSLAILLGVAFCWAPYSLSFTIVLSFYSSATGPKSVWTRIAFWLQWNSFVNPLLYPL 360
 QY 361 CHKRFOKAPLKIFCIKKOPLPSQHSRSVSS 390
 DB 361 CHKRFOKAPLKIFCIKKOPLPSQHSRSVSS 390

RESULT 8

ABB78276 standard; protein; 390 AA.
 ID ABB78276

AC ABB78276;
 XX
 XX

DT 05-DEC-2002 (first entry)

DE Amino acid sequence of human histamine receptor.

XX Human; histamine receptor; receptor; inflammation; asthma; allergy;
 KW atopic dermatitis; stroke; myocardial infarction; migraine;
 KW chronic obstructive pulmonary disease; COPD; rheumatoid arthritis;
 KW multiple sclerosis; inflammatory bowel disease; psoriasis;
 KW intracellular second messenger pathway; cellular growth rate;
 KW hormone secretion.

XX Homo sapiens.

PN US2002098539-A1.

PD 25-JUL-2002.

PF 19-MAR-2001; 2001US-00812216.

PR 07-OCT-1999; 99US-00414010.

XX (BEHA/) BEHAN J X.
 PA (HEDR/) HEDRICK J A.
 PA (LAZT/) LAZ T M.
 PA (MONS/) MONSMA F J.
 PA (MORS/) MORSE K L.
 PA (UMLA/) UMLAND S P.
 PA (WANG/) WANG S.

PI Bahan JX, Hedrick JA, Laz TM, Monsma FJ, Morse KL, Umland SP;
 PI Wang S;

DR WPI; 2002-673827/72.
 DR N-PSDB; ABW78739.
 PT Novel mammalian histamine receptor polypeptide useful for identifying
 PT agonist or antagonist for treating diseases such as inflammation, asthma,
 PT stroke, migraine, rheumatoid arthritis, multiple sclerosis, psoriasis.
 XX
 PS Claim 2; Page 16-17; 21pp; English.
 CC The present sequence represents a histamine receptor. The polypeptide is
 CC useful for identifying an agonist or antagonist of a mammalian histamine
 CC receptor. It is useful as an antigen to elicit the production of
 CC antibodies. The histamine receptor polypeptide and polynucleotide are
 CC useful in the treatment and management of diseases such as inflammation,
 CC asthma, allergy, atopic dermatitis, stroke, myocardial infection,
 CC migraine, chronic obstructive pulmonary disease (COPD), rheumatoid
 CC arthritis, multiple sclerosis, inflammatory bowel disease and psoriasis.
 CC They are also useful for modulating intracellular second messenger
 CC pathway activated through histamine receptors (cyclic-AMP, calcium,
 CC inositol phosphate and mitogen activated protein (MAP) kinase), changes
 CC in cellular growth rate, secretion of hormones, receptor-stimulated Ca²⁺
 CC mobilization, mitogenic effects, etc
 XX
 SQ Sequence 390 AA;
 Query Match 100.0%; Score 2024; DB 5; Length 390;
 Best Local Similarity 100.0%; Pred. No. 1.5e-211;
 Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPDNTSTINSLSTRVTLAFPMSLVAFALMGALVTLAFVVDKRLRHRSYFFLNLALS 60
 DB 1 MPDNTSTINSLSTRVTLAFPMSLVAFALMGALVTLAFVVDKRLRHRSYFFLNLALS 60
 QY 61 DFEVGVISIPLYIPHTLFEMDFGKEICVFWLTTDYLLCTASVYNIIVLISYDRYLSVNAV 120
 DB 61 DFEVGVISIPLYIPHTLFEMDFGKEICVFWLTTDYLLCTASVYNIIVLISYDRYLSVNAV 120
 QY 121 SYRTQHTGVAKITLVAVVAVLAFVNGPMILVSEMKDGSCEPQFSEWYTLATTSF 180
 DB 121 SYRTQHTGVAKITLVAVVAVLAFVNGPMILVSEMKDGSCEPQFSEWYTLATTSF 180
 QY 121 LEFVIVILVAVFNNNIYMSLWKRDLHSLRCQSHPLGLTAVSNICGHSFGRSLSSRLSLA 240
 DB 121 LEFVIVILVAVFNNNIYMSLWKRDLHSLRCQSHPLGLTAVSNICGHSFGRSLSSRLSLA 240
 QY 181 LEFVIVILVAVFNNNIYMSLWKRDLHSLRCQSHPLGLTAVSNICGHSFGRSLSSRLSLA 240
 DB 181 LEFVIVILVAVFNNNIYMSLWKRDLHSLRCQSHPLGLTAVSNICGHSFGRSLSSRLSLA 240
 QY 241 STEVPASFHSERQRKSSLMFSSRTKNSNTIASKMGSFQSDSVALLHOREHELLRAR 300
 DB 241 STEVPASFHSERQRKSSLMFSSRTKNSNTIASKMGSFQSDSVALLHOREHELLRAR 300
 QY 301 LAKSLAILLGAVFVAVCAVPSLFTIIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPLLYPL 360
 DB 301 LAKSLAILLGAVFVAVCAVPSLFTIIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPLLYPL 360
 QY 361 CHRFQKAFIKTFCIKKQPLPSQHSRSVSS 390
 DB 361 CHRFQKAFIKTFCIKKQPLPSQHSRSVSS 390

XX
 EN W0200192485-A1.
 XX
 PD 06-DEC-2001.
 XX
 PF 22-FEB-2001; 2001WO-US005914.
 XX
 PR 31-MAY-2000; 2000US-0208260P.
 XX
 PA (ORTH) ORTHO-MCNEIL PHARM INC.
 XX
 PI Lovenberg T, Liu C;
 XX
 DR WPI; 2002-114339/15.
 DR N-PSDB; AAT70980.
 XX
 PS Claim 13; Fig 2; 92pp; English.
 CC The present sequence is that of a human histamine receptor of the H4
 CC subtype, as predicted from a cDNA clone isolated from a bone marrow cDNA
 CC library. The invention provides mammalian (human, mouse, rat and guinea
 CC pig) histamine H4 receptor nucleic acid molecules (see AAT70980-83) and
 CC polypeptides (see AAM50564-67). The nucleic acids have been expressed in
 CC recombinant host cells that produce active recombinant protein. The
 CC pharmacology of known histamine ligands is demonstrated. Mammalian
 CC histamine H4 receptor may be used in gene therapy for the treatment of
 CC diseases where it is beneficial to elevate mammalian histamine H4
 CC receptors activity. Recombinant protein is useful for identifying
 CC modulators of the human histamine H4 receptor. Such modulators may be
 CC useful for diagnosing, treating or preventing asthma, allergy,
 CC inflammation, cardiovascular and cerebrovascular disorders, non-insulin
 CC dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia,
 CC disorders of the neuroendocrine system, stress and spasticity
 XX
 SQ Sequence 390 AA;
 Query Match 100.0%; Score 2024; DB 5; Length 390;
 Best Local Similarity 100.0%; Pred. No. 1.5e-211;
 Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPDNTSTINSLSTRVTLAFPMSLVAFALMGALVTLAFVVDKRLRHRSYFFLNLALS 60
 DB 1 MPDNTSTINSLSTRVTLAFPMSLVAFALMGALVTLAFVVDKRLRHRSYFFLNLALS 60
 QY 61 DFEVGVISIPLYIPHTLFEMDFGKEICVFWLTTDYLLCTASVYNIIVLISYDRYLSVNAV 120
 DB 61 DFEVGVISIPLYIPHTLFEMDFGKEICVFWLTTDYLLCTASVYNIIVLISYDRYLSVNAV 120
 QY 121 SYRTQHTGVAKITLVAVVAVLAFVNGPMILVSEMKDGSCEPQFSEWYTLATTSF 180
 DB 121 SYRTQHTGVAKITLVAVVAVLAFVNGPMILVSEMKDGSCEPQFSEWYTLATTSF 180
 QY 121 LEFVIVILVAVFNNNIYMSLWKRDLHSLRCQSHPLGLTAVSNICGHSFGRSLSSRLSLA 240
 DB 121 LEFVIVILVAVFNNNIYMSLWKRDLHSLRCQSHPLGLTAVSNICGHSFGRSLSSRLSLA 240
 QY 181 LEFVIVILVAVFNNNIYMSLWKRDLHSLRCQSHPLGLTAVSNICGHSFGRSLSSRLSLA 240
 DB 181 LEFVIVILVAVFNNNIYMSLWKRDLHSLRCQSHPLGLTAVSNICGHSFGRSLSSRLSLA 240
 QY 241 STEVPASFHSERQRKSSLMFSSRTKNSNTIASKMGSFQSDSVALLHOREHELLRAR 300
 DB 241 STEVPASFHSERQRKSSLMFSSRTKNSNTIASKMGSFQSDSVALLHOREHELLRAR 300
 QY 301 LAKSLAILLGAVFVAVCAVPSLFTIIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPLLYPL 360
 DB 301 LAKSLAILLGAVFVAVCAVPSLFTIIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPLLYPL 360
 QY 361 CHRFQKAFIKTFCIKKQPLPSQHSRSVSS 390
 DB 361 CHRFQKAFIKTFCIKKQPLPSQHSRSVSS 390

RESULT 10
 AAC66023.
 ID AAG66023 standard; protein; 390 AA.
 XX
 AC AAG66023;
 DT 27-FEB-2002 (first entry)
 XX
 DE Human histamine H4 receptor protein.
 XX
 KW Histamine receptor; H4; antirheumatic; antiarthritic; immunosuppressive;
 KW antiallergic; antiallergic; neuroprotective; antidiabetic; human;
 KW cerebroprotective; CAMP modulator; gene therapy.
 XX
 OS Homo sapiens.
 XX
 FT Key Location/Qualifiers
 FT Domain 12..40 /note= "transmembrane domain"
 FT Domain 52..69 /note= "transmembrane domain"
 FT Domain 88..110 /note= "transmembrane domain"
 FT Domain 130..154 /note= "transmembrane domain"
 FT Domain 172..196 /note= "transmembrane domain"
 FT Domain 304..325 /note= "transmembrane domain"
 FT Domain 342..362 /note= "transmembrane domain"
 FT Domain /note= "transmembrane domain"
 XX
 PN MO200185786-A2.
 XX
 PD 15-NOV-2001.
 XX
 PF 04-MAY-2001; 2001MO-US014527.
 XX
 PR 05-MAY-2000; 2000US-0202151P.
 PR 23-AUG-2000; 2000US-0227567P.
 PR 13-NOV-2000; 2000US-0247855P.
 XX
 PA (AMHP) AMERICAN HOME PROD CORP.
 XX
 PI Jones PG, Blatcher M, Wu S, Pausch MH;
 XX
 DR WPI: 2002-049442/06.
 DR N-PSDB; AA167750.
 XX
 PT New histamine receptor, termed H4 useful for detecting H4 (ant)agonists
 PT for treating transplanted organ rejection, asthma, allergy, multiple
 PT sclerosis and rheumatoid arthritis.
 XX
 PS Claim 5; Fig 1; 66pp; English.
 XX
 CQ The invention provides an isolated histamine receptor, H4, which binds
 CQ ligands comprising imidazole attached to amine by an alkyl chain. The H4
 CQ receptor can be expressed by standard recombinant methodology. Cells
 CQ expressing H4 receptor protein at a detectable level can suppress cyclic
 CQ adenosine monophosphate (cAMP) formation when contacted with the H4
 CQ receptor agonist. The H4 receptor and antibodies are used for identifying
 CQ H4 receptor modulators. Modulation of histamine H4 receptors is useful
 CQ for treating transplanted organ rejection, asthma, allergies and
 CQ autoimmune pathologies such as multiple sclerosis, type I diabetes,
 CQ rheumatoid arthritis, cognitive and memory defects. The H4 receptor
 CQ protein and nucleic acids are useful targets to identify drugs that are
 CQ effective in treating disorders associated with histamine-regulated
 CQ processes. Identification and isolation of H4 receptor provides for
 CQ development of screening of molecules that interact with H4 receptors.
 CQ Genetic variants of H4 can be used to diagnose an H4 associated disease
 CQ as described above. The H4 receptor polynucleotide is useful to treat or
 CQ prevent a disorder associated with the function of H4 in peripheral blood
 CQ leukocytes. The present sequence represents the human histamine H4

CC receptor protein
 XX
 SQ Sequence 390 AA;
 Query Match 100.0%; Score 2024; DB 5; Length 390;
 Best Local Similarity 100.0%; Pred. No. 1.5e-211;
 Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPDNTSTINISLSTRVTLAFPMSLVAFPAIMLGNALVILAFVVDKXLRHRSYFPPLALIS 60
 DB 1 MPDNTSTINISLSTRVTLAFPMSLVAFPAIMLGNALVILAFVVDKXLRHRSYFPPLALIS 60
 QY 61 DFEVGIISLPLYPHLTFEEDGKEICVFWLTDTDLCTASVNYILISYDRLYSNAY 120
 DB 61 DFEVGIISLPLYPHLTFEEDGKEICVFWLTDTDLCTASVNYILISYDRLYSNAY 120
 QY 121 SYRTQHTGVLYKIVTLVAVVLAFLVNGPMILVSESMDGSECEGPFSEWYILAITSF 180
 DB 121 SYRTQHTGVLYKIVTLVAVVLAFLVNGPMILVSESMDGSECEGPFSEWYILAITSF 180
 QY 181 LEFVIVILVAVYNNNIYSLMKRDHLSCQSHPGILTAVSNICGHSFGRSLSSRSLSA 240
 DB 181 LEFVIVILVAVYNNNIYSLMKRDHLSCQSHPGILTAVSNICGHSFGRSLSSRSLSA 240
 QY 241 STEVPASFSHERRRKSSLSMESRTKNSNTIASKMGSPSQSDSVLHOREHYELLRAR 300
 DB 241 STEVPASFSHERRRKSSLSMESRTKNSNTIASKMGSPSQSDSVLHOREHYELLRAR 300
 QY 301 IAKSLAILLGVPVAVCAVPSLFTIVLSFYSSATGPKSVWYRIAFWLQWPNFVNPPLLYPL 360
 DB 301 IAKSLAILLGVPVAVCAVPSLFTIVLSFYSSATGPKSVWYRIAFWLQWPNFVNPPLLYPL 360
 QY 361 CHRRFQKAFKIFCIKKOPLPSQHSRSVS 390
 DB 361 CHRRFQKAFKIFCIKKOPLPSQHSRSVS 390
 RESULT 11
 AAU74906
 ID AAU74906 standard; protein; 390 AA.
 XX
 AC AAU74906;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE Amino acid sequence of human G-protein coupled receptor TGR62 protein.
 XX
 KW Human; G-protein coupled; receptor; GPCR; TGR62; kidney disease;
 KW signal transduction modulator; cerebral cavernous malformation;
 KW hyperlipidemia; obesity; dyslexia; cardiac myxoma; renal failure;
 KW nephritis; hypertension; liver disease; cirrhosis; blood disorder;
 KW spleen-associated disorder; immune disorder.
 XX
 OS Homo sapiens.
 XX
 PN MO200200719-A2.
 XX
 PD 03-JAN-2002.
 XX
 PF 25-JUN-2001; 2001MO-US020363.
 XX
 PR 23-JUN-2000; 2000US-0213461P.
 XX
 PA (TULA-) TULARIX INC.
 XX
 PI Lin DC, Zhao J, Chen J, Cutler G;
 XX
 DR WPI: 2002-147880/19.
 DR N-PSDB; ABK12959.
 XX
 PT New G-protein coupled receptor polypeptides, useful for identifying
 PT modulators of signal transduction for treating kidney disease,
 PT hyperlipidemia, obesity, dyslexia and cardiac myxoma.

XX Claim 26, Page 61, 78pp; English.

PS The present invention relates to a new G-protein coupled receptor (GPCR)

CC polypeptide comprising greater than 70% amino acid sequence identity to

CC the amino acid sequence of human GPCRs TGR2, TGR21, TGR30.1, TGR30.2,

CC human TGR13 or TGR92, 80% amino acid sequence identity to mouse TGR18 or

CC 90% amino acid sequence identity to human novel ecd receptor protein, as

CC defined in the specification. The GPCR covalently linked to a solid phase

CC is useful for identifying a compound that modulates signal transduction.

CC The identified compounds are useful for treating kidney disease, cerebral

CC cavernous malformations, hyperlipidemia, obesity, dyslexia and cardiac

CC myxoma. The molecules of the invention are useful for diagnosing

CC disorders or conditions such as kidney-related conditions or diseases

CC such as renal failure, nephritis, nephrotic syndrome, asymptomatic

CC urinary abnormalities, renal tubule defects, hypertension and

CC nephrolithiasis, liver-related disease or condition e.g. cirrhosis,

CC infiltrations, lesions, functional disorders and jaundice and spleen-

CC associated disorders or conditions e.g. splenic enlargement, immune

CC disorders, blood disorders and others. Modulation of the polypeptide of

CC the invention is useful to treat or prevent any of the above conditions

CC or diseases. The present amino acid sequence represents the human GPCR

CC TGR62 protein of the invention. This sequence is one of seven novel G

CC protein coupled receptors of the invention (AAU74904- AAU74911)

XX

SO Sequence 390 AA;

Query Match 100.0%; Score 2024; DB 5; Length 390;

Best Local Similarity 100.0%; Pred. No. 1.5e-211; Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPDNTNINSLSTRVLAFAFMVAFAIMGNLVLIAFVADKRLRRHSYFLNLAIS 60

DB 1 MPDNTNINSLSTRVLAFAFMVAFAIMGNLVLIAFVADKRLRRHSYFLNLAIS 60

QY 61 DFEVGVISILYIPHTLFEMDFEKEICVFMTLDYLLCTASVNIIVLISDRYISVNAV 120

DB 61 DFEVGVISILYIPHTLFEMDFEKEICVFMTLDYLLCTASVNIIVLISDRYISVNAV 120

QY 121 SYRTOHGVKIVTLVAVVLAFLVNGPMILVSEMKDESECEPGEFSEWYLLATTSF 180

DB 121 SYRTOHGVKIVTLVAVVLAFLVNGPMILVSEMKDESECEPGEFSEWYLLATTSF 180

QY 181 LEFVPIVILVAFNMNIYSLMKRDLSPCCSHPGTLAVASNNICGHFRRGLSRRSLA 240

DB 181 LEFVPIVILVAFNMNIYSLMKRDLSPCCSHPGTLAVASNNICGHFRRGLSRRSLA 240

QY 241 STEVPAFSEHERORRKSIMFSSRTKNSNTIASKMGFSQSDVALHOREHVELLRAR 300

DB 241 STEVPAFSEHERORRKSIMFSSRTKNSNTIASKMGFSQSDVALHOREHVELLRAR 300

QY 301 LAASLAILLGVAVCAVPYSLFTIVLSFYSSATGPKSVWRIAFWLOWNFSFVNPLLYPL 360

DB 301 LAASLAILLGVAVCAVPYSLFTIVLSFYSSATGPKSVWRIAFWLOWNFSFVNPLLYPL 360

QY 361 CRRKFOKAFKICFKICOPLPSSOHSRVS 390

DB 361 CRRKFOKAFKICFKICOPLPSSOHSRVS 390

RESULT 12

ABG71960 ID ABG71960 standard; protein; 390 AA.

XX AC ABG71960;

XX DT 28-JAN-2003 (first entry)

XX DE Human G-protein coupled receptor AXOR35.

XX KW Human; receptor; G-protein coupled receptor; AXOR35; lymphocyte; macrophage; eosinophil; neutrophil; infection; transplant rejection; gastrointestinal disorder; gastric ulcer; inflammatory bowel disease;

KW Crohn's disease; irritable bowel syndrome; vomiting; inflammation; atopic dermatitis; allergy; autoimmune disorder; rheumatoid arthritis; psoriasis; urological disease; urinary retention; cardiovascular disease; myocardial infarction; hypotension; hypertension; pulmonary disorder; chronic obstructive pulmonary disease; cough; renal disease; renal ischaemia; arteriosclerosis; atherosclerosis; psychosis; neurological disorder; migraine; anorexia; anxiety; schizophrenia; dyskinesia; Parkinson's disease; cancer; obesity; stroke; septic shock; graft versus host disease; osteoporosis.

OS Homo sapiens.

XX US2002137054-A1.

PN 26-SEP-2002.

XX 20-JUL-2001; 2001US-00910411.

PF 02-NOV-1999; 99US-00431898.

PR 03-FEB-2000; 2000US-00497790.

PR 20-OCT-2000; 2000US-00693761.

XX (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.

PI Aubart KM, Bergema DJ, Fitzgerald L, Graybill TL, Li X;

PI Michalovich D, Morrow DM, Zhu Y;

DR WPI, 2003-074982/07.

DR N-PSDB; ABS57063.

XX Novel isolated G-protein coupled receptor polypeptide, AXOR35, useful for treating infections, gastrointestinal disorders autoimmune disorders, urological diseases, cardiovascular diseases and cancer.

PT

XX Claim 1, Page 22, 24pp; English.

PS The invention relates to an isolated G-protein coupled receptor polypeptide, AXOR35, (and its homologues, variants, complements and RNA equivalents). Also included are an anti-AXOR35 antibody, an AXOR35 expression vector, producing a recombinant host cell by introducing the vector into a cell such that the host cell produces AXOR35, a membrane of the host cell expressing AXOR35, identifying/screening for agonists or antagonists of AXOR35 and inhibiting or promoting the function of lymphocytes, macrophages, eosinophils, or neutrophils in diseased tissue, by administering to the patient AXOR35 agonists or antagonists. The agonist or antagonist identified is useful for treating a disease such as asthma, or for inhibiting or promoting the function of lymphocytes, macrophages, eosinophils, or neutrophils in diseased tissue such as an asthmatic lung. AXOR35 or polynucleotide is useful in diagnostic assays, for identifying compounds that are agonists or antagonists of AXOR35, as vaccines, or for treating infections (bacterial, fungal, protozoan or viral infections), transplant rejection, gastrointestinal disorders (such as gastric ulcer), inflammatory bowel diseases (such as Crohn's disease), irritable bowel syndrome, vomiting, inflammation (such as atopic dermatitis), allergy, autoimmune disorders (such as rheumatoid arthritis, psoriasis), urological diseases (such as urinary retention), cardiovascular diseases (such as myocardial infarction), hypotension, hypertension, pulmonary disorders (such as chronic obstructive pulmonary disease), cough, renal diseases (such as renal ischaemia), arteriosclerosis, atherosclerosis, psychotic and neurological disorders (such as migraine, anorexia, anxiety, schizophrenia), dyskinesias (such as Parkinson's disease), cancer, obesity, stroke, septic shock, graft versus host disease and osteoporosis. The present sequence represents human AXOR35

XX

SO Sequence 390 AA;

Query Match 100.0%; Score 2024; DB 6; Length 390;

Best Local Similarity 100.0%; Pred. No. 1.5e-211; Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MPDNTNSTINLSLSTRVTLAFMSLVAFAMLGNALVILAFVVDKRLRRSSFFFLNLAIS 60
DB 1 MPDNTNSTINLSLSTRVTLAFMSLVAFAMLGNALVILAFVVDKRLRRSSFFFLNLAIS 60
QY 61 DFFGVGISIPLYIPHTLFEMDFGKEICVFWMLTDDYLCTASVYNIIVLISYDRYLSVSNV 120
DB 61 DFFGVGISIPLYIPHTLFEMDFGKEICVFWMLTDDYLCTASVYNIIVLISYDRYLSVSNV 120
QY 121 SYRTOHTGVKIVTLMAVAVLAVNGPMILVSESMKDESGECPGFSEMYILATISF 180
DB 121 SYRTOHTGVKIVTLMAVAVLAVNGPMILVSESMKDESGECPGFSEMYILATISF 180
QY 181 LEFVTPVILVAVFNNNIYMSLMKRDHLSCQSHPELTAVSSNICGHSFRGLSSRRSLISA 240
DB 181 LEFVTPVILVAVFNNNIYMSLMKRDHLSCQSHPELTAVSSNICGHSFRGLSSRRSLISA 240
QY 241 STEVPASFSHERORRKSLSMFSSRTKNNSNTIASKMSFQSDSVLAHQREHVELLRARR 300
DB 241 STEVPASFSHERORRKSLSMFSSRTKNNSNTIASKMSFQSDSVLAHQREHVELLRARR 300
QY 301 LAKSLAILLGVAFCVAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPLLYPL 360
DB 301 LAKSLAILLGVAFCVAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPLLYPL 360
QY 361 CHKRFOKAFKIFCIKKQPLPSQHSRSVSS 390
DB 361 CHKRFOKAFKIFCIKKQPLPSQHSRSVSS 390

```

RESULT 13

ABU92265
ID ABU92265 standard; protein; 390 AA.

XX AC ABU92265;

XX DT 16-JUL-2003 (first entry)

XX DE Human G protein-coupled receptor hRUP7.

XX KW Human; receptor; orphan G protein-coupled receptor; GPCR; hARE-3; hARE-4;
KW hARE-5; hRUP3; hRUP6; hRUP7; hGPCR27; hARE-1; hARE-2; hPR1; hG2A;
KW hGHN3; hGHN4; hGHN6; hGHN8; hGHN9; hGHN10; hRUP4; signalling cascade.

XX OS Homo sapiens.

XX PN US2003017528-A1.

XX PD 23-JAN-2003.

XX PF 06-JUN-2001; 2001US-00875076.

XX PR 20-NOV-1998; 98US-0109213P.
PR 16-FEB-1999; 99US-0120416P.
PR 26-FEB-1999; 99US-0121852P.
PR 12-MAR-1999; 99US-0123946P.
PR 12-MAR-1999; 99US-0123946P.
PR 28-MAY-1999; 99US-0136436P.
PR 28-MAY-1999; 99US-0136437P.
PR 28-MAY-1999; 99US-0136439P.
PR 28-MAY-1999; 99US-0136567P.
PR 28-MAY-1999; 99US-0137127P.
PR 28-MAY-1999; 99US-0137131P.
PR 29-JUN-1999; 99US-014448P.
PR 28-SEP-1999; 99US-0156333P.
PR 29-SEP-1999; 99US-0156555P.
PR 29-SEP-1999; 99US-0156634P.
PR 12-OCT-1999; 99US-00417044.

XX PA (CHEN/) CHEN R.
PA (DANG/) DANG H T.
PA (LIAM/) LIAM C W.
XX PA (LINI/) LIN I.

PI Chen R, Dang HT, Liam CW, Lin I;
XX WPI; 2003-428952/40.
DR N-PSDB; ACA93262.
XX Novel endogenous, orphan, human G protein-coupled receptors useful for
PT identification of modulators of the receptor and as research tools for
PT understanding the role of the receptor in human body.

XX Claim 26; Page 23; 54pp; English.

CC The invention relates to a human G protein-coupled receptor (GPCR)
CC appearing as ABU92259-ABU92277 (encoded by cDNAs ACA93256-ACA93274) named
CC hARE-3, hARE-4, hARE-5, hRUP3, hRUP6, hRUP7, hGPCR27, hARE-1, hARE
CC -2, hPR1, hG2A, hGHN3, hGHN4, hGHN6, hGHN8, hGHN9, hGHN10 and hRUP4.
CC Also included are a plasmid comprising a vector and one of the cDNAs
CC above and a host cell comprising the plasmid. The GPCRs are useful for
CC the direct identification of candidate compounds as inverse agonists,
CC agonists or partial agonists. In vitro and in vivo systems incorporating
CC GPCRs is useful for elucidating and understanding the roles these
CC receptors play in the human condition, both normal and diseased, as well
CC as understanding the role of constitutive activation as it applies to
CC understanding the signalling cascade. The cDNAs are useful for making a
CC probe for dot-blot analysis against tissue mRNA and/or RT-PCR
CC identification of the expression of the receptor in tissue samples. The
CC present sequence represents a GPCR of the invention

XX Sequence 390 AA;

Query Match 100.0%; Score 2024; DB 6; Length 390;

Best Local Similarity 100.0%; Pred. No. 1.5e-211; Indels 0; Gaps 0;

Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MPDNTNSTINLSLSTRVTLAFMSLVAFAMLGNALVILAFVVDKRLRRSSFFFLNLAIS 60
DB 1 MPDNTNSTINLSLSTRVTLAFMSLVAFAMLGNALVILAFVVDKRLRRSSFFFLNLAIS 60
QY 61 DFFGVGISIPLYIPHTLFEMDFGKEICVFWMLTDDYLCTASVYNIIVLISYDRYLSVSNV 120
DB 61 DFFGVGISIPLYIPHTLFEMDFGKEICVFWMLTDDYLCTASVYNIIVLISYDRYLSVSNV 120
QY 121 SYRTOHTGVKIVTLMAVAVLAVNGPMILVSESMKDESGECPGFSEMYILATISF 180
DB 121 SYRTOHTGVKIVTLMAVAVLAVNGPMILVSESMKDESGECPGFSEMYILATISF 180
QY 181 LEFVTPVILVAVFNNNIYMSLMKRDHLSCQSHPELTAVSSNICGHSFRGLSSRRSLISA 240
DB 181 LEFVTPVILVAVFNNNIYMSLMKRDHLSCQSHPELTAVSSNICGHSFRGLSSRRSLISA 240
QY 241 STEVPASFSHERORRKSLSMFSSRTKNNSNTIASKMSFQSDSVLAHQREHVELLRARR 300
DB 241 STEVPASFSHERORRKSLSMFSSRTKNNSNTIASKMSFQSDSVLAHQREHVELLRARR 300
QY 301 LAKSLAILLGVAFCVAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPLLYPL 360
DB 301 LAKSLAILLGVAFCVAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPLLYPL 360
QY 361 CHKRFOKAFKIFCIKKQPLPSQHSRSVSS 390
DB 361 CHKRFOKAFKIFCIKKQPLPSQHSRSVSS 390

```

RESULT 14

ABP81727
ID ABP81727 standard; protein; 390 AA.

XX AC ABP81727;

XX DT 04-MAR-2003 (first entry)

XX DE Human histamine H4 receptor protein SEQ ID NO:629.

XX KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;

KM G protein-coupled receptor modulator; antibody; immune-related disease;
 KM growth-related disease; cell regeneration-related disease; AIDS; cancer;
 KM immunological-related cell proliferative disease; autoimmune disease;
 KM Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 KM osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
 KM graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KM psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KM mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KM hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 KM ulcer.
 KM Homo sapiens.
 XX MO200261087-A2.
 XX 08-AUG-2002.
 XX 19-DEC-2001; 2001MO-US050107.
 XX 19-DEC-2000; 2000US-0257144P.
 XX (LIFE-) LIFESPAN BIOSCIENCES INC.
 XX Burner GC, Roush CL, Brown JP;
 XX WPI, 2003-046718/04.
 XX N-PSDB; AB242573.
 XX New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR), useful for diagnosing and designing drugs for treating conditions
 PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
 PT autoimmune diseases.
 XX Disclosure; Fig 1; 523pp; English.
 XX The present invention describes antigenic peptides (i) comprising: (a)
 CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 CC acids. Also described: (1) an assay for the detection of a particular G
 CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity or
 CC avidity for a particular GPCR. (i) can be used as GPCR modulators and in
 CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
 CC antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related disease, immunological-related cell proliferative
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention
 XX Sequence 390 AA:
 SQ
 Query Match 100.0%; Score 2024; DB 6; Length 390;
 Best Local Similarity 100.0%; Pred. No. 1,5e-211;
 Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPDNTNINISLSTRTVLAFFMSVLAFAIMGNLVIAFYVDKRLRRSSYFFLNTAIS 60
 DB 1 MPDNTNINISLSTRTVLAFFMSVLAFAIMGNLVIAFYVDKRLRRSSYFFLNTAIS 60
 QY 61 DFFPGVISIPYIPIHTLFEMDPGKEICVFWLTDDYLLCTASVYNIIVLISYRYSVSNV 120

DB 61 DFFPGVISIPYIPIHTLFEMDPGKEICVFWLTDDYLLCTASVYNIIVLISYRYSVSNV 120
 QY 121 SYRTQHTGVLTQYTLMAVAVVLAFLVNGPMILVSESKDECEBEPFPFSWYLLATISF 180
 DB 121 SYRTQHTGVLTQYTLMAVAVVLAFLVNGPMILVSESKDECEBEPFPFSWYLLATISF 180
 QY 181 LEFVPIVLAFAFMNINYSMLMKRDHLSCOSHPGLTAVSNICGHSFGRSLSSRRSLSA 240
 DB 181 LEFVPIVLAFAFMNINYSMLMKRDHLSCOSHPGLTAVSNICGHSFGRSLSSRRSLSA 240
 QY 241 STEVPASFSHERQRKSSLMFSSRTKNSNTIASIKWGSFQSQDSVALHOREHVELLRAR 300
 DB 241 STEVPASFSHERQRKSSLMFSSRTKNSNTIASIKWGSFQSQDSVALHOREHVELLRAR 300
 QY 301 LAKSLAILLGVPVCAVPYSLFTIVLSFYSSAGPKSVWTRIAFWLQWPNFSFVNPPLYPL 360
 DB 301 LAKSLAILLGVPVCAVPYSLFTIVLSFYSSAGPKSVWTRIAFWLQWPNFSFVNPPLYPL 360
 QY 361 CHKRFOKAPLKFICIKKQPLPSQHSRVS 390
 DB 361 CHKRFOKAPLKFICIKKQPLPSQHSRVS 390
 RESULT 15
 AAE36417
 ID AAE36417 standard; protein: 390 AA.
 XX AAE36417;
 AC AAE36417;
 DT 07-AUG-2003 (first entry)
 XX Human H4 receptor wild-type protein #2.
 XX Human; H4; histamine receptor; inflammatory bowel disease; psoriasis;
 KM atopic dermatitis; stroke; myocardial infarction; migraine; allergy;
 KM chronic obstructive pulmonary disease; COPD; cerebroprotective; therapy;
 KM rheumatoid arthritis; multiple sclerosis; inflammation; neuroprotective;
 KM asthma; receptor.
 XX Homo sapiens.
 XX MO2003020907-A2.
 XX 13-MAR-2003.
 XX 30-AUG-2002; 2002MO-US027891.
 XX 31-AUG-2001; 2001US-0316762P.
 XX 13-NOV-2001; 2001US-0332697P.
 XX (MERI) MERCK & CO INC.
 XX Gallagher MJ, Yates SL;
 DR WPI, 2003-290186/28.
 DR N-PSDB; AAD55126.
 PT Novel splice variants of human H4 histamine receptor, H4b and H4c, useful
 PT for identifying agonists or antagonists of the receptor which are useful
 PT for treating multiple sclerosis, asthma, allergy, psoriasis and stroke.
 XX Example; Page 58-60; 31pp; English.
 XX The invention relates to splice variants of human H4 histamine receptor,
 CC H4b and H4c. The invention is useful for identifying an agonist, the
 CC antagonist or inverse agonist of a mammalian histamine receptor. The
 CC agonist, antagonist or inverse agonist of H4b and H4c is useful for
 CC treating inflammation, asthma, allergy, atopic dermatitis, stroke,
 CC myocardial infarction, migraine, chronic obstructive pulmonary disease
 CC (COPD), rheumatoid arthritis, multiple sclerosis, inflammatory bowel
 CC disease, or psoriasis. The present sequence is human H4 receptor protein
 XX Sequence 390 AA.
 SQ

Query Match	100.0%;	Score 204;	DB 6;	Length 390;
Best Local Similarity	100.0%;	Pred. No. 1.5e-211;		
Matches 390;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	MPDNTSNTINSLSTRVTLAFPMFSLVFAFALMGALVTLAFVVDKOLRRRSSYFFLNLAIS	60
Db	1	MPDNTSNTINSLSTRVTLAFPMFSLVFAFALMGALVTLAFVVDKOLRRRSSYFFLNLAIS	60
QY	61	DFEFGVISIPLYI PHTLFEMDFGKEICVFMLTTDYLLCTASVYNIVLISYDRYLSVSNV	120
Db	61	DFEFGVISIPLYI PHTLFEMDFGKEICVFMLTTDYLLCTASVYNIVLISYDRYLSVSNV	120
QY	121	SYRTORTGVLYITLVAAVWVTLAFVNGGMILVSSWDEGECGPGFFSFWYLLATTSF	180
Db	121	SYRTORTGVLYITLVAAVWVTLAFVNGGMILVSSWDEGECGPGFFSFWYLLATTSF	180
QY	181	LEFVYPIVILVAYFNNMIYVSLMKRDLHSRCOSHPLGTAVSNMICHSFEGELSRRLSLA	240
Db	181	LEFVYPIVILVAYFNNMIYVSLMKRDLHSRCOSHPLGTAVSNMICHSFEGELSRRLSLA	240
QY	241	STEVPA SFHSERORRKS LMFSSRTMNSNTIASKXGSPQSDVALHQREHVELLRARR	300
Db	241	STEVPA SFHSERORRKS LMFSSRTMNSNTIASKXGSPQSDVALHQREHVELLRARR	300
QY	301	LASLAILLGVFAVCAPYSLFTIYLSFSSATGPKSVWYRAAFLOMFNSFVNPPLYPL	360
Db	301	LASLAILLGVFAVCAPYSLFTIYLSFSSATGPKSVWYRAAFLOMFNSFVNPPLYPL	360
QY	361	CHKRPOKAFKICIKKOPLPSSHRSVSS 390	
Db	361	CHKRPOKAFKICIKKOPLPSSHRSVSS 390	

Search completed: March 28, 2006, 13:54:32Z
Job time : 190 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Ran on: March 28, 2006, 13:54:50 ; Search time 40 Seconds
(without alignments)
938.113 Million cell updates/sec

Title: US-10-616-088-2
Perfect score: 2024
Sequence: 1 MPDINSTINSLSTRVTLAF.....KIFCIKKQPLPSQHSRSVSS 390

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 9621673 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR 80: *
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2024	100.0	390	2 JC7566	histamine H4 recep
2	432	21.3	639	2 A55019	muscarinic acetyl
3	415	20.5	590	2 S01114	muscarinic acetyl
4	413	20.4	590	2 S47572	muscarinic acetyl
5	411	20.3	590	2 S10128	muscarinic acetyl
6	409	20.2	589	2 B29514	muscarinic acetyl
7	408	20.2	589	2 A29476	muscarinic acetyl
8	406.5	20.1	589	2 S58868	G protein-coupled
9	402.5	19.9	515	2 A40491	alpha-1-adrenergic
10	399.5	19.7	517	2 A45121	alpha-1B adrenergic
11	393.5	19.4	379	2 JC6178	serotonin receptor
12	392.5	19.4	515	2 JC1525	alpha-1B-adrenergic
13	392.5	19.3	2	2 JC70530	muscarinic acetyl
14	391.5	19.3	460	2 I51837	muscarinic recepto
15	391.5	19.3	460	2 A29514	muscarinic acetyl
16	391	19.3	460	2 A24325	muscarinic acetyl
17	390	19.3	491	2 A41632	histamine H1 recep
18	388	19.2	460	2 S09508	muscarinic acetyl
19	387	19.1	466	2 A27386	muscarinic acetyl
20	386	19.1	466	2 S10126	muscarinic acetyl
21	386	19.1	486	2 JC1415	histamine H1 recep
22	385.5	19.0	531	2 UT0531	muscarinic acetyl
23	384.5	19.0	501	2 T18863	hypothetical prote
24	381	18.8	466	2 A40972	muscarinic acetyl
25	380.5	18.8	477	2 S71323	alpha-1A adrenergic
26	379.5	18.8	488	2 I56507	histamine H1 recep
27	379.5	18.8	466	2 JC10197	muscarinic acetyl
28	377.5	18.7	429	2 S65656	alpha-1C-adrenergic
29	377.5	18.7	466	2 UN0765	alpha-1C-adrenergic

30	377.5	18.7	499	2 S65657	alpha-1C-adrenergic
31	376.5	18.6	466	2 S10856	muscarinic acetyl
32	375.5	18.6	460	2 A31897	muscarinic acetyl
33	373.5	18.5	476	2 JC5042	G protein-coupled
34	372.5	18.4	390	2 JN0268	serotonin receptor
35	372.5	18.4	466	2 A35375	alpha-1-adrenergic
36	372.5	18.4	466	2 I57959	alpha-1C adrenergic
37	372	18.4	487	2 JC2495	histamine H1 recep
38	370	18.3	444	1 DYB02	dopamine receptor
39	369.5	18.3	501	2 JH0447	alpha-1A-adrenergic
40	369.5	18.3	572	2 I39369	alpha-1A-adrenergic
41	367.5	18.2	377	2 A53269	serotonin receptor
42	366.5	18.1	366	2 A47321	serotonin receptor
43	366.5	18.1	601	2 JH0170	octopamine recepto
44	366	18.1	444	1 DYMSD2	dopamine receptor
45	366	18.1	444	1 S08146	dopamine receptor

ALIGNMENTS

RESULT 1

JC7566 histamine H4 receptor, HH4R - human
C/Species: Homo sapiens (man)
C/Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C/Accession: JC7566
R:Nakamura, T.; Itadani, H.; Hidaka, Y.; Ohta, M.; Tanaka, K.
Biochem. Biophys. Res. Commun. 279, 615-620, 2000
A/Title: Molecular cloning and characterization of a new human histamine receptor, HH4R
A/Reference number: JC7566; MUID: 20568725; PMID:1118334
A/Contents: Leukocyte
A/Accession: JC7566
A/Molecule type: mRNA
A/Residues: 1-390 <NR>
A/Cross-references: UNIPROT:Q9H3N8; UNIPARC:UPI0000039A92; DDBJ:AB045370
C/Comment: This receptor, belonging to the biogenic amine receptors of G protein-couple
C/Genetics:
A/Gene: hh4r
C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match	Score 2024;	DB 2;	Length 390;
Beat Local Similarity	100.0%;	Pred. No.3.1e-162;	
Matches 390;	Conservative 0;	Mismatches 0;	Indels 0;
Gaps 0;			
QY	1	MPDINSTINSLSTRVTLAFNLSVAPAIMGNALVTLAFVVDKMLRRSSYFLNLAIS 60	
DB	1	MPDINSTINSLSTRVTLAFNLSVAPAIMGNALVTLAFVVDKMLRRSSYFLNLAIS 60	
QY	61	DFPVGVISIPLYIPHTLFEWDPGKEICVFWLTTDYLLCTASVTNIVLISDRYLSVSNV 120	
DB	61	DFPVGVISIPLYIPHTLFEWDPGKEICVFWLTTDYLLCTASVTNIVLISDRYLSVSNV 120	
QY	121	SYRQHTGULKIYTLMAVAVVLAFLVNGPMILVSESKDGSCEPPEFSEWYLTATSF 180	
DB	121	SYRQHTGULKIYTLMAVAVVLAFLVNGPMILVSESKDGSCEPPEFSEWYLTATSF 180	
QY	121	SYRQHTGVAKIYTLMAVAVVLAFLVNGPMILVSESKDGSCEPPEFSEWYLTATSF 180	
DB	121	SYRQHTGVAKIYTLMAVAVVLAFLVNGPMILVSESKDGSCEPPEFSEWYLTATSF 180	
QY	181	LEFVPIVLAIVFNMNIYVSLMKRDHLSCOSHPGLAVASNNICGHSFRRLSSRRSLSA 240	
DB	181	LEFVPIVLAIVFNMNIYVSLMKRDHLSCOSHPGLAVASNNICGHSFRRLSSRRSLSA 240	
QY	181	LEFVPIVLAIVFNMNIYVSLMKRDHLSCOSHPGLAVASNNICGHSFRRLSSRRSLSA 240	
DB	181	LEFVPIVLAIVFNMNIYVSLMKRDHLSCOSHPGLAVASNNICGHSFRRLSSRRSLSA 240	
QY	241	STEVPAFHSERORRKSLLMFSSRTTQNSNTIASKWSFQSDSVALLHOREVELLPARR 300	
DB	241	STEVPAFHSERORRKSLLMFSSRTTQNSNTIASKWSFQSDSVALLHOREVELLPARR 300	
QY	241	STEVPAFHSERORRKSLLMFSSRTTQNSNTIASKWSFQSDSVALLHOREVELLPARR 300	
DB	241	STEVPAFHSERORRKSLLMFSSRTTQNSNTIASKWSFQSDSVALLHOREVELLPARR 300	
QY	301	LAKSLATLGVPAVCAPVSLFTIVLSFYSSATGSPSVWYRIAPWLQMPNSFVNPLLYPL 360	
DB	301	LAKSLATLGVPAVCAPVSLFTIVLSFYSSATGSPSVWYRIAPWLQMPNSFVNPLLYPL 360	
QY	361	CHKRFOKAFKICIKKQPLPSQHSRSVSS 390	
DB	361	CHKRFOKAFKICIKKQPLPSQHSRSVSS 390	

RESULT 2

A55019

muscarinic acetylcholine receptor, M3 isoform - chicken

C:Species: Gallus gallus (chicken)

C:Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 09-Jul-2004

C:Accession: A55019

R:Gadbut, A.P.; Galper, J.B.

J. Biol. Chem. 269, 25823-25829, 1994

A:Title: A novel M-3 muscarinic acetylcholine receptor is expressed in chick atrium and

A:Reference number: A55019; MUID:95014393; PMID:7922827

A:Accession: A55019

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-639 <GND>

A:Cross-references: UNIPROT:P49578; UNIPARC:UPI00001252B4; GB:L10617; NID:G530097; PIDN:

C:Superfamily: vertebrate rhodopsin

C:Keywords: neurotransmitter receptor

Query Match 21.3%; Score 432; DB 2; Length 639;

Best Local Similarity 23.0%; Pred. No. 2,2e-28;

Matches 126; Conservative 92; Mismatches 151; Indels 180; Gaps 15;

QY 4 TNSITNLSLSTR-----VTIAFMSLVAFALMGALVITLAFVVDKRLRRSSYFF 54
 DB 96 TNSILNATIKDPLGHAVMQVLLAFLTGILALVTIIGNILIVSFKVKNKQLKTVNNYFL 155
 QY 55 LNLAIISDFVVISIPIYPTLTF-EMDFGKEICVFMLTDTYLLCTASVNVIVLISYDRY 113
 DB 156 LSLACADLIIVISNLTFTYITIGHMALGNLACDLWLSIDVSNASVNMVLIVISPRY 215
 QY 114 LSVNNAVSYRTOHGTGLKIVTLMAV--VTLAFVNGPMILVSESMDGS---ECEBGF 168
 DB 216 FSIRPLPLYRAKRT--TRAGVMIGLAWISFVLAAPAILFMQYVFGKTVPLDECFIOF 273
 QY 169 FSEWYIATISFLEVLIVIVLVAIFNNIYSLMKRDLSCQSHPGITAVSSNICGSHF 228
 DB 274 LSEPIIFFGTIAAFYLLVFTIISI---LYRIYKETE-KTKELAGLQASGESEATARF 328
 QY 229 RGRISRSRLSASTEVPAASFSESRORRKSLSL-----FSS 263
 DB 329 VHQGSSRSLS-----SYELQROSTRSSRRKTRCHFWLTKMSWEPNTDQGDHSS 381
 QY 264 RTKNSNTIASKM----- 276
 DB 382 SDSNNNDAAASLENSASSDEEDITAFETRAIYSIVLKPGHSAILNSTKLPSSSEDLNESA 441
 QY 277 -----GSFQO-----SPSVA----- 286
 DB 442 DELQSDTDSQEKPKQLQPKSIODGGSFOKSFSLPIOPGSAETATASDGISSTVTKTS 501
 QY 287 -----LHOREVELLRARLAKSLAILLGFVACMAFYSFLT 323
 DB 502 AALPLSFKEATLAKKFAKTRSQITKRRMSLIKKAQTLISALFPIITWPNINMV 561
 QY 324 IVLSFYSSATSPKSVWYRIAFMLQWFSFVNPLVPLCHKRFQKAFKIF---CIKQPL 380
 DB 562 LVNFFCDGV--PKTYW-NLGYWLCYINSTVPCYALCNKRFNTPFKQLLLCQCDKRRGR 618
 QY 381 PSQHSRSVS 389
 DB 619 KQOYQOROS 627

RESULT 3
 S01114
 muscarinic acetylcholine receptor M2, glandular - pig
 N:Alternate names: muscarinic acetylcholine receptor III
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
 C:Accession: S01114
 R:AKida, I.; Kudo, T.; Meda, A.; Bujo, H.; Nakai, J.; Mishina, M.; Numa, S.
 FEBS Lett. 235, 257-261, 1988

A:Title: Primary structure of porcine muscarinic acetylcholine receptor III and antagonist

A:Reference number: S01114; MUID:88296835; PMID:3402600

A:Accession: S01114

A:Molecule type: DNA

A:Residues: 1-590 <AKI>

A:Cross-references: UNIPROT:P11483; UNIPARC:UPI00001252B7; EMBL:X12712; NID:G1861; PIDN

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmembrane

F:68-91/Domain: transmembrane #status predicted <TM1>

F:105-125/Domain: transmembrane #status predicted <TM2>

F:143-164/Domain: transmembrane #status predicted <TM3>

F:185-207/Domain: transmembrane #status predicted <TM4>

F:231-252/Domain: transmembrane #status predicted <TM5>

F:493-513/Domain: transmembrane #status predicted <TM6>

F:528-546/Domain: transmembrane #status predicted <TM7>

Query Match 20.5%; Score 415; DB 2; Length 590;

Best Local Similarity 24.3%; Pred. No. 5,4e-27;

Matches 126; Conservative 88; Mismatches 151; Indels 154; Gaps 15;

QY 16 VTIAFMSLVAFALMGALVITLAFVVDKRLRRSSYFFLNLAIISDFVVISIPIYTPH 75
 DB 69 VETIAFLTGILALVTIIGNILIVAFVKNKQLKTVNNYFLISLACADLIIVISNLTFTY 128
 QY 76 TLP-EMDFGKEICVFMLTDTYLLCTASVNVIVLISYDRYLSNNAVSYRTOHGTGLKIVT 134
 DB 129 INNRMALGNLACDLWLSIDVSNASVNMVLIVISPRYSIRPLPYRAKRT--TRAG 186
 QY 135 LMAV--VTLAFVNGPMILVSESMDGS---ECEBGFSEWYIATISFLEFVPIVL 189
 DB 187 VMIGLAWISFVLAAPAILFMQYVFGKTVPLDECFIOFSEPIITFTGTIAAFVMPVTI 246
 QY 190 VAYFNNIYVSLMKRDLSCQSHPGITAVSSNICGSHFGRLSRSLS----- 239
 DB 247 MTI---LYRIYKETE-KTKELAGLQASGESEATARFVHPGSSRSCTSYELQOQSLK 301
 QY 240 -----ASTEPASFSRQRKS 257
 DB 302 RSARKRYRCHFWFTTSKWPASAEQMDQDSSDSNNNDAAASLENSASSDEEDITSET 361
 QY 258 SLWFS-----SRTKNSN-----TI-----ASKM-----GSFS 280
 DB 362 RAITSIVLKPGHSITLNSITKLPSSDNLQVPEBELGTVDERASLKQQAQSMDDGSFQ 421
 QY 281 QSDS-----VALHQREHV 293
 DB 422 KSPFKPIQESAVDTAKASDVNSVSGKTATPLPSFEKATLAKRFALKTRSQITKRRKM 481
 QY 294 ELRARLALSLAILLGVPAVCAPYSLFTIVLSFYSATAGPSWYRIAFMLQWFSFV 353
 DB 482 SLIKERKAQTLISALIAFIIITWPNINMVNTPFCDSCI-PKTYW-NLGYWLCYINSTV 539
 QY 354 NPLLYPCHKRFQKAFKIF---CIKQPLPSQHSRSVS 389
 DB 540 NPVCYALCNTRFTTFKQLLLCQCDKRRKQYQOROS 578

RESULT 4
 S47572
 muscarinic acetylcholine receptor m3 - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
 C:Accession: S47572
 R:Lee, P.H.K.; Hodges, P.K.; Glickman, F.; Chang, K.J.
 Biochim. Biophys. Acta 1223, 151-154, 1994
 A:Title: Cloning and expression of a cDNA encoding bovine muscarinic acetylcholine m3 r
 A:Reference number: S47572; MUID:94339178; PMID:8061048
 A:Accession: S47572
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-590 <LEB>
 A:Cross-references: UNIPROT:P41984; UNIPARC:UPI00001252B3; EMBL:U08286; NID:G520465; PI
 C:Superfamily: vertebrate rhodopsin


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Db      115  ORWVFGVVCWMLTCTDVLCTASTLNCALADRYATITPINTYAKRT--LRVLANIA 173
      138  AVWVLAFLVNGPMILVSEWKEGSECEPFSE--WYIIATISFLFVIVLVAENM 195
      174  GVMILSGVSSPPIGNMDWMEFNDTTPCQLTGQGVV--YSLGSPFILLFIMTYIV 232
Qy      196  NIYVS---LKKRDLHSCQS---HGLTVSSNICHSRGRGLSRRLSASTE--- 243
      233  EIFIATRRRLERKAKASTLNSAMKQMAQAQVSPSPSH--DQESVSETHNEL 285
      244  ---VPASFSEERORRKSLSL----- 260
      286  PPPAPSPSKERKRTKKSKKQEAERGLAPAMVAEDSVTNSVSGVPAANHAE 345
      261  -FSSRTKNSNT-----IASKMGFS-----QSDSVALHQ---REVELLRA 298
      346  GYCTCTTTTTTTTAAVDSPRSRTASQKSTAPTPVPQPSIPVQPIEEKRISLSKE 405
Qy      299  RRLAKSLAILLGVAVCAPISLFTIVLSFYSSATGPKSVWYRIAFWLQMFNSFVNP 358
      406  RRAARTLGIIMGVVVCMLPFELMYIVFPCNPCKSPKLVNFTIMLGYNLSALNP 465
      359  PLCHRFQKAFKIFCTK 376
      466  TTFMLDRRAFKLLHFK 483

```

RESULT 9

A40491
 alpha-1-adrenergic receptor - golden hamster
 C/Species: Mesocricetus auratus (golden hamster)
 C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
 C/Accession: A40491
 R/Cotechta, S.; Schim, D.A.; Randall, R.R.; Lefkowitz, R.J.; Caron, M.G.; Kobilka, B.
 Proc. Natl. Acad. Sci. U.S.A. 85, 7159-7163, 1988
 A/Title: Molecular cloning and expression of the cDNA for the hamster alpha-1-adrenergic
 A/Reference number: A40491; MUID:8901157; PMID:2845398
 A/Molecule type: mRNA
 A/Residues: 1-515 <COT>
 A/Cross-references: UNIPROT:P18841; UNIPARC:UPI0000124FC9; GB:J04084; NID:G619407; PIDN:
 C/Superfamily: vertebrate rhodopsin
 C/Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein

```

Query Match      19.9%; Score 402.5; DB 2; Length 515;
Best Local Similarity 28.4%; Pred. No. 5.1e-26;
Matches 107; Conservative 83; Mismatches 132; Indels 55; Gaps 14;

Qy      4  TNSTI-NLSISTRYTLAFM-SLVAFAIMGNALVILAFVVDKNLRRSSYFLNLAISD 61
      33  SNSTLPQLDITRAISVGLVGAFLIPAI-VGNILVILSVACNHLRPTNYFIVNLAMAD 91
      62  FFGVVISIPLYIP-HTLFEMDPGKEICVFWLITDYLCTASVNIIVLISYDRIVSNAV 120
      92  LILSTFVLPSPALBVLGWLKRIFCDIWAANDVLCCTASISLCAISIDRYIGVYSL 151
      121  SYRTOHTGVKITYTLWAAVWLAFLVN-GPMILVSEWKEGSECEPFSEWYIATIS 179
      152  QYFTLVTR-RKAILALISVWLVSTVSIQPLGKKEPAPDDKEC--GYTEEPYALFSS 208
      180  FLEFVIP--VILVAYFMNIIYMSLMKRDHLSRCQSHRGLTAIVSSNICHSFRGLSSRRS 237
      209  LGSFYIPLAVILVMY-----CRVYIVAKRTTKNL-----EAGYMK 244
      238  LSASTEVPASFSEERORRKSLSLMSRTKNS--NTIASKMGFSQSDSVALHQREHVEL 295
      245  MNSSKETLTRIHSKNFHEDT--LSSTKAGHNPRSSIAVGLKFS----- 287
      296  LRARRLAKSLAILLGVAVCAPISLFTIVLSFYSSATGPKSVWYRIAFWLQMFNSFVNP 355
      288  -REKKAATIGIYVGMFIICMLPFELMYIVFPCNPCKSPKLVNFTIMLGYNLSALNP 345

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```

Qy      356  LLYPLCHKRFQKAFK 372
      346  ILYPCSSKEFRKAFMR 362

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RESULT 10

A45121
 alpha-1B adrenergic receptor - human
 C/Species: Homo sapiens (man)
 C/Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
 C/Accession: A45121; J02332
 R/Ramirez, C.S.; Denker, J.M.; Perez, D.M.; Galvin, R.J.; Riek, R.P.; Graham, R.M.
 J. Biol. Chem. 267, 21936-21945, 1992
 A/Title: Genomic organization and expression of the human alpha 1B-adrenergic receptor.
 A/Reference number: A45121; MUID:93016158; PMID:1328250
 A/Accession: A45121
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-517 <RAM>
 A/Cross-references: UNIPROT:P35368; UNIPARC:UPI0000149ED4; GB:M99590; NID:G176211
 A/Note: Sequence extracted from NCBI backbone (NCBI:P116785)
 A/Note: this translation is not annotated in GenBank entry HUMADRENH, release 113.0 #da
 R/Weinberg, D.H.; Trivedi, P.; Tan, C.P.; Mitra, S.; Perkins-Barrow, A.; Borkowski, D.;
 Biochem. Biophys. Res. Commun. 201, 1296-1304, 1994
 A/Title: Cloning, expression and characterization of human alpha adrenergic receptors a
 A/Reference number: J02331; MUID:94296402; PMID:8024574
 A/Accession: J02332
 A/Molecule type: mRNA
 A/Residues: 1-158; 'P', 160-244, 'H', 246-314, 'F', 316-380, 382-517 <WEI>
 A/Cross-references: UNIPARC:UPI00001778AA
 C/Genetics:
 A/Gene: GDB:ADRA1B
 A/Cross-references: GDB:127901; OMIM:104220
 A/Map position: 5q31.1-5q33.2
 C/Superfamily: vertebrate rhodopsin
 C/Keywords: G protein-coupled receptor; transmembrane protein
 F/33-72/Domain: transmembrane #status predicted <TM1>
 F/81-111/Domain: transmembrane #status predicted <TM2>
 F/121-146/Domain: transmembrane #status predicted <TM3>
 F/157-184/Domain: transmembrane #status predicted <TM4>
 F/203-227/Domain: transmembrane #status predicted <TM5>
 F/280-320/Domain: transmembrane #status predicted <TM6>
 F/326-360/Domain: transmembrane #status predicted <TM7>

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Query Match      19.7%; Score 399.5; DB 2; Length 517;
Best Local Similarity 28.1%; Pred. No. 9.2e-26;
Matches 106; Conservative 84; Mismatches 132; Indels 55; Gaps 14;

Qy      4  TNSTI-NLSISTRYTLAFM-SLVAFAIMGNALVILAFVVDKNLRRSSYFLNLAISD 61
      33  SNSTLPQLDITRAISVGLVGAFLIPAI-VGNILVILSVACNHLRPTNYFIVNLAMAD 91
      62  FFGVVISIPLYIP-HTLFEMDPGKEICVFWLITDYLCTASVNIIVLISYDRIVSNAV 120
      92  LILSTFVLPSPALBVLGWLKRIFCDIWAANDVLCCTASISLCAISIDRYIGVYSL 151
      121  SYRTOHTGVKITYTLWAAVWLAFLVN-GPMILVSEWKEGSECEPFSEWYIATIS 179
      152  QYFTLVTR-RKAILALISVWLVSTVSIQPLGKKEPAPDDKEC--GYTEEPYALFSS 208
      180  FLEFVIP--VILVAYFMNIIYMSLMKRDHLSRCQSHRGLTAIVSSNICHSFRGLSSRRS 237
      209  LGSFYIPLAVILVMY-----CRVYIVAKRTTKNL-----EAGYMK 244
      238  LSASTEVPASFSEERORRKSLSLMSRTKNS--NTIASKMGFSQSDSVALHQREHVEL 295
      245  MNSSKETLTRIHSKNFHEDT--LSSTKAGHNPRSSIAVGLKFS----- 287
      296  LRARRLAKSLAILLGVAVCAPISLFTIVLSFYSSATGPKSVWYRIAFWLQMFNSFVNP 355
      288  -REKKAATIGIYVGMFIICMLPFELMYIVFPCNPCKSPKLVNFTIMLGYNLSALNP 345
      356  LLYPLCHKRFQKAFK 372

```

Db 346 IYPCSSKEFKAFARI 362

RESULT 11

JC6178

serotonin receptor - Barnacle

N/Alternate names: 5-hydroxytryptamine receptor (5-HT)

C/Species: Balanus amphitrite (barnacle)

C/Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004

C/Accession: JC6178

R/Kawahara, H.; Isoai, A.; Shizuri, Y.

Gene 184, 245-250, 1997

A/Title: Molecular cloning of a putative serotonin receptor gene from barnacle, Balanus

A/Reference number: JC6178; MUID:97183669; PMID:9031635

A/Accession: JC6178

A/Molecule type: DNA

A/Residues: 1-379 <KAM>

A/Cross-references: UNIPROT:Q9J127; UNIPARC:UPI000012BA93; DDBJ:D83547; NID:g1507660; PI

C/Comment: This is a G-protein-coupled receptor.

C/Superfamily: octopamine receptor type I

C/Keywords: disulfide bond; neurotransmitter receptor; transmembrane protein

Query Match 19.4%; Score 393.5; DB 2; Length 379;
Best Local Similarity 25.7%; Pred. No. 2.1e-25;

Matches 98; Conservative 89; Mismatches 160; Indels 35; Gaps 9;

2 PDNSTI-----NLSLSTRVTLAFPMISLAFAMLMGNLVILAFVVDKNLRHRSYFPLN 56

Db 14 PELNASAPLDDEBELGETVAATALLAILLVTVGNLSLVISVTPYRPLASVGNFFVVS 73

QY 57 LAISDFVGVISIPLYIPHTLF-EMDFGKEICVFMVLTDDYLLCTASVNIIVLISDYRLS 115

Db 74 LAVADLTVALFVLPVLAAYVRLNOMLGLSGSYLCOMMLTCDICCTSSINLTCVIALDRYMA 133

QY 116 VSNMVSRTQHTGVLYKTYLWVAVVWVLAFLVNGPMILVSESMKDGSCGCEGFSEWYIL 175

Db 134 ITDDINAAQKRT-IRRVMTMAAVWALSIVISVPELLEMDNDMPDFTDTCCTLOERLIF 192

QY 176 AI-TSFLFVIVLVILVAYFNNIYWSLWKRDHLSRQSHPLGLTVSSNICHSFGRSLSS 234

Db 193 VYSSSGSFPIPLIMSVYAKIFPATRR--LAERTKLGTLVNPAP-----PQRSS 244

QY 235 RRSLSASTEVPAFSHSEKRRKSSLMFSSRTKMSNTIASKMGFSQSDSVALHQ----R 290

Db 245 RP--LAELSVASQEDETEPSPPEPLSSRADKPPAN-----GISVHQFIEEK 289

QY 291 EHVLLARRLAKSLAILLGVAVCMAPYSLEFIVLSFYSSATGPKSVWYRIAFMLQWEN 350

Db 290 QRISLSEKKAARVYGVIMGVVCMVLPFFLMYALVPECTNCAPPSQKRVVDVFTWLGYN 349

QY 351 SFVNPVLVPLCHKRFQKAFLEKI 372

Db 350 SSINPIITYITINQKPRTFRSL 371

RESULT 12

JC1525

alpha-1B-adrenergic receptor - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004

C/Accession: JC1525; S08400

R/Gao, B.; Kunos, G.

Gene 131, 243-247, 1993

A/Title: Isolation and characterization of the gene encoding the rat alpha 1B adrenergic

A/Reference number: JC1525; MUID:94010315; PMID:8406017

A/Accession: JC1525

A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-515 <GAO>

A/Cross-references: UNIPROT:P15823; UNIPARC:UPI0000170842; GB:L08610; NID:G202624; PIDN:

R/Votig, M.M.; Kieper, J.; Chin, H.

Nucleic Acids Res. 18, 1053, 1990

A/Title: Sequence of a rat brain cDNA encoding an alpha-1B adrenergic receptor.

A/Reference number: S08400; MUID:90192094; PMID:2156222

A/Accession: S08400

A/Molecule type: mRNA

A/Residues: 1-202, 'C', 204-206, 'C', 208-305, 'C', 307-414, 'OK', 417-439, 'C', 441-483, 'ATA', 48

A/Cross-references: UNIPARC:UPI0000154878; EMBL:X51585; NID:955557; PIDN:CA435934.1; PI:

C/Genetics: 317/1

C/Introns: vertebrate rhodopsin

C/Superfamily: vertebrate rhodopsin

C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 19.4%; Score 392.5; DB 2; Length 515;

Best Local Similarity 28.1%; Pred. No. 3.6e-25;

Matches 106; Conservative 83; Mismatches 133; Indels 55; Gaps 14;

4 TNSIT-NLSLSTRVTLAFPM-SLAFAMLMGNLVILAFVVDKNLRHRSYFPLNLAISD 61

Db 33 SNSITLPQDVTBRAISVGLVIGAFILFAL-VGNILVILSVACNRHLRPTVYFIVNLAIAD 91

QY 62 PFVGVISIPLYIP-HTLFENDFGKEICVFMVLTDDYLLCTASVNIIVLISDYRLSVNAV 120

Db 92 LLSPFVLPPSARTLEVGVWVLRIFCDIWAADVLCCTASILSLCAISIDRYIGVYSL 151

QY 121 SYRQHTGVLYKTYLWVAVVWVLAFLVN-GPMILVSESMKDGSCGCEGFSEWYILAIYS 179

Db 152 QYPLVTR-RKAILALISVWLSVISTGFLGKKEAPAPDDDEC--GVTEEPYALFSS 208

QY 180 FLEFVID--YILVAYFNNIYWSLWKRDHLSRQSHPLGLTVAVSNTICHSFGRSLSSRS 237

Db 209 LGSEYIPLAIVLVWY-----CRVYIVAKRTTKNL-----EAGVWKE 244

QY 238 LSASTEVPAFSHSEKRRKSSLMFSSRTKMS--NTIASKMGFSQSDSVALHREHVEL 295

Db 245 MSMSKELTLRHISGNFIEDT--LSSTPAKGNPSSIAVXLPFS----- 287

QY 296 LRARLLKSLAILLGVAVCMAPYSLEFIVLSFYSSATGPKSVWYRIAFMLQWENFVNP 355

Db 288 -REKKAATIGIVGNMILSLPFLALPLGLSLFTLKPPDAV-FKVPFHLGYNSCLNP 345

QY 356 LLYPLCHKRFQKAFLEKI 372

Db 346 IYPCSSKEFKAFARI 362

RESULT 13

JT0530

muscarinic acetylcholine receptor M5 - human

C/Species: Homo sapiens (man)

C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 21-Jan-2000

C/Accession: JT0530

R/Bonner, T.I.; Young, A.C.; Brann, M.R.; Buckley, N.J.

Neuron 1, 403-410, 1988

A/Title: Cloning and expression of the human and rat m5 muscarinic acetylcholine recept

A/Reference number: JT0530; MUID:90165521; PMID:3272174

A/Accession: JT0530

A/Molecule type: DNA

A/Residues: 1-532 <BON>

A/Cross-references: UNIPARC:UPI00001778C4

C/Comment: Muscarinic acetylcholine receptors mediate many of the actions of the neuro

C/Superfamily: vertebrate rhodopsin

C/Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosph

F/30-53/Domain: transmembrane #status predicted <TM1>

F/67-87/Domain: transmembrane #status predicted <TM2>

F/105-126/Domain: transmembrane #status predicted <TM3>

F/147-169/Domain: transmembrane #status predicted <TM4>

F/192-214/Domain: transmembrane #status predicted <TM5>

F/444-464/Domain: transmembrane #status predicted <TM6>

F/479-498/Domain: transmembrane #status predicted <TM7>

F/8.13/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.4%; Score 392.5; DB 2; Length 532;

Best Local Similarity 22.6%; Pred. No. 3.7e-25;

Matches 110; Conservative 89; Mismatches 156; Indels 131; Gaps 14;

```

QY 16 VTLAFPMSLVAFAMLSNALVTLAFVVDKNLHRSSEYFELNALISDFEYVVISIPLXPH 75
DB 31 ITLAALVAVVSLITIVGNLVMSIFKVNLSQKLTAVNYLSLACADLLSGIFSMNLVTTY 90
QY 76 TLV-F-EWDFGKEICVFWLTTDYLLCTASVYNYLVISYDRLSVSNVSYRTOHTGLXIVT 134
DB 91 ILMGRMLGSLACDMLADLDYASNAVNNLVISFDRFSTIRPLTYRAKTP--KXAG 148
QY 135 LMAVAV-WTLAFVNGPMILVSESMKDEGS---ECPGFSSWYLLAITSFLEPIYIVIL 189
DB 149 IMIGLAWLISFILWAPAILCQYLVGKRTVPLEDCOIOFLSEPTITFGTALAFYIPVS 208
QY 190 VAYFNNMNY----- 198
DB 209 MTILYCRITRETEKTKOLADLQSSDSVTKAEKKRRPAHRAFRSCLRCPRPTLAQERNQ 268
QY 199 --WSP-----W-KRDLRSRCSHPG-----LTAV 219
DB 269 ASWSSSRSTSTGKPSQATGPSANWAKAEQLTTCSSVPSSEDEKPAITDVLQVYVYSQ 328
QY 220 SSNIGHSFRGLSRSLASTE-----VPSFHSERORRKSILMFSSRTYON 268
DB 329 GKESRGEFFSAEETEETVKAEETKSDYDTPNYLLSPAARPKSQKCAVAKFRLVVRAD 388
QY 269 SN-----TIASKMGs--FQSDSVLHQRHVELLARRLAKSLAILL 309
DB 389 GNOETNNGCHKVKIMPCPPVAKKEPSTGLNPNPHQTKRRVVLVXERKAAQTLAIL 448
QY 310 GVFAVCWAPYSLFTVLFSYSATGPKSVWYRIAFMLQMFNSFVPLLYPLCHKRFQKAF 369
DB 449 LAFTITTPYIMLVSTFCDKCV-PVTLMH-LGTYMLCVANSTVNPICVYALCNRFRTTF 506
QY 370 -LKIFC 374
DB 507 KMLILC 512

RESULT 14
151837
muscarinic receptor - rat
C/Species: Rattus sp. (rat)
C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 24-Nov-1999
C/Accession: 151837
R/Idat, J.; Smith, T.L.; Mei, L.; Ikeda, M.; Fujiwara, Y.; Gomez, J.; Halonen, M.; Roeske
Adv. Exp. Med. Biol. 287, 333-330, 1991
A/Title: The molecular properties of the M1 muscarinic receptor and its regulation of cy
A/Reference number: 151837; MUID:92101806; PMID:1759615
A/Accession: 151837
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-460 <RES>
A/Cross-references: UNIPARC:UPI0000046CE7; GB:S73971; NID:9241253; PIDN:AAB20705.1; PID:
C/Genetics:
A/Genes: ml
C/Superfamily: vertebrate rhodopsin

Query Match 19.3%; Score 391.5; DB 2; Length 460;
Best Local Similarity 25.8%; Pred. No. 3.8e-25;
Matches 121; Conservative 84; Mismatches 149; Indels 115; Gaps 19;

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QY 166 PGFSEWYLLAITSFLEFVILVAVFNNMNYSLMKRD-----HLRCSQSH--PGLTA 218
DB 180 IQFLSQPLITGTMAAFYLPVTWC-----TLVKRIRHETNRAELALQGSFPGKG 235
QY 219 VSSNICGHSFRGLSRSLRST--LSASTEVA-----SFHSERORRKSIL 259
DB 236 GSSS-----SSERSQCGAGESPSPGRCRCRCCAPRLLOAYSMKEEEDSGSM 285
QY 260 --MFSRTKSNSTIASMGSPQSOSDYA----- 286
DB 286 ESLTSSBGEBSGVVTKM---PMVDEQAAPTQPKSPNTYKRPYKKGRDRGKQK 342
QY 287 -----LHOREHVELLARRLAKSLAILGVFAVCWAPYSLFTVLFSYSATGPKSVWY 340
DB 343 PRGKEQLAKRTPLSEVKKAAKTLAILAFILTPYIMLVSTFCDKCV-PETIM- 400
QY 341 RIAFWLQMFNSFVNPPLLYPLCHKRFQKAF-LKIFC-----IKQOP 379
DB 401 ELGYWLCVNSTVNPVCYALCNKAFRDTFRLLLCRWDKRRMRKIPKRP 449

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RESULT 15
A29514
muscarinic acetylcholine receptor M1 - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C/Accession: A94518; A94293; A37121; A29514
R/Bonner, T.I.
Submitted to GenBank, July 1987
A/Reference number: A94518
A/Accession: A94518
A/Molecule type: mRNA
A/Residues: 1-460 <BO1>
A/Cross-references: UNIPROT:P08482, UNIPARC:UPI0000046CE7
R/Bonner, T.I.; Buckley, N.J.; Young, A.C.; Bram, M.R.
Science 237, 527-532, 1987
A/Title: Identification of a family of muscarinic acetylcholine receptor genes.
A/Reference number: A94293; MUID:87263421; PMID:3037705
A/Accession: A94293
A/Molecule type: mRNA
A/Residues: 1-227,338-460 <BO2>
A/Cross-references: UNIPARC:UPI00001778CE; UNIPARC:UPI00001778CF
A/Note: Experimental source: cerebral cortex
A/Note: Only a part of the protein translation is given; none of the nucleotide sequenc
R/Kuttenbach, E.; Cutler, C.A.M.; Pedder, E.K.; Aitken, A.; Harris, A.C.M.; Hulme, E.C.
J. Biol. Chem. 265, 13702-13708, 1990
A/Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues inv
A/Reference number: A37121; MUID:90337982; PMID:2380182
A/Accession: A37121
A/Status: preliminary
A/Molecule type: protein
A/Residues: 62-124 <RUR>
A/Cross-references: UNIPARC:UPI00001778D0
C/Superfamily: vertebrate rhodopsin
C/Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosp
F:25-50/Domain: transmembrane #status predicted <TM1>
F:62-93/Domain: transmembrane #status predicted <TM2>
F:100-121/Domain: transmembrane #status predicted <TM3>
F:142-168/Domain: transmembrane #status predicted <TM4>
F:187-209/Domain: transmembrane #status predicted <TM5>
F:367-387/Domain: transmembrane #status predicted <TM6>
F:402-420/Domain: transmembrane #status predicted <TM7>
F:2.12/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.3%; Score 391.5; DB 2; Length 460;
Best Local Similarity 25.8%; Pred. No. 3.8e-25;
Matches 121; Conservative 84; Mismatches 149; Indels 115; Gaps 19;

```


GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 28, 2006, 13:51:30 ; Search time 233 Seconds.

(without alignments)
1180.927 Million cell updates/sec

Title: US-10-616-088-2

Perfect score: 2024
Sequence: 1 MPDNTNINLSLSTRTVTLAF.....KIFCIKQPLPSCHRSRVSS 390

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2024	100.0	390	1 HRH4 HUMAN	O913N8 homo sapien
2	2024	100.0	390	2 O4G0T6 HUMAN	O4G0T6 homo sapien
3	2016	99.6	390	2 O961D9 HUMAN	O961D9 homo sapien
4	1436.5	71.0	390	2 O8WNV9 PIG	O8WNV9 sus scrofa
5	1413.5	69.8	391	2 O91ZY1 RAT	O91ZY1 rattus norv
6	1377.5	68.1	391	2 O91ZY2 MOUSE	O91ZY2 mus musculus
7	1318.5	65.1	389	2 O91ZY3 CAVPO	O91ZY3 cavia porce
8	889	43.9	175	2 O6U9U5 PANTR	O6U9U5 pan troglod
9	882	43.6	174	2 O6U9U4 PERIM	O6U9U4 gorilla gor
10	730	36.1	445	2 O865E1 MACMU	O865E1 macaca mlla
11	729	36.0	445	1 HRH3 RAT	O91YU8 rattus norv
12	727	35.9	445	1 HRH3 MOUSE	P58406 mus musculus
13	727	35.9	445	2 O540B3 MOUSE	O540B3 mus musculus
14	727	35.9	445	2 O5G535 PHOSU	O5G535 phodopus su
15	726.5	35.9	445	1 HRH3 CAVPO	O91135 cavia porce
16	724	35.8	445	1 HRH3 HUMAN	O915M1 homo sapien
17	724	35.8	445	2 O548M6 HUMAN	O548M6 homo sapien
21	700.5	34.6	341	2 O4RVG9 TETNG	O4RVG9 tetradon n
22	693.5	34.3	473	2 O6ZM33 BRARE	O6ZM33 brachydanio
23	693	34.2	406	2 O5G534 PHOSU	O5G534 phodopus su
24	673	33.3	365	2 O8WY01 HUMAN	O8WY01 homo sapien
25	673	33.3	373	2 O8WY02 HUMAN	O8WY02 homo sapien
26	563	27.8	344	2 O5PPG3 RAT	O5PPG3 rattus norv
27	488.5	24.1	301	2 O8WY00 HUMAN	O8WY00 homo sapien
28	488.5	24.1	309	2 O8N149 HUMAN	O8N149 homo sapien
29	440	21.7	401	2 O4RLR2 TETNG	O4RLR2 tetradon n
30	432.5	21.4	475	2 O5TLF2 PNEOP	O5TLF2 papilio xut
31	432	21.3	639	1 ACM3_CHICK	P45578 gallus gall

32	430.5	21.3	477	1 OAR_HELVI	O25188 heliothis v
33	430.5	21.3	527	2 O5END7 LEPMW	O5END7 lepomis mac
34	430	21.2	399	2 O9NG02 APIME	O9NG02 apis mellif
35	425.5	21.0	477	2 O9BMA9 TAMBW	O9BMA9 mamestra br
36	425.5	21.0	639	2 O5MBW9 COLLI	O5MBW9 colomba liv
37	421	20.8	584	2 O61W39 CAEBR	O61W39 caenorhabdi
38	417.5	20.6	587	2 O8VH26 CAVPO	O8VH26 cavia porce
39	416.5	20.6	490	2 O7T286 BRARE	O7T286 brachydanio
40	415	20.5	580	1 ACM3_PIG	P11483 sus scrofa
41	415	20.5	611	1 ACM3_CABEL	O9U765 caenorhabdi
42	413	20.4	590	1 ACM3_BOVIN	P41964 bos taurus
43	411	20.3	590	1 ACM3_HUMAN	P20309 homo sapien
44	411	20.3	590	1 ACM3_PONPY	O9N2A2 pongo pygma
45	411	20.3	590	2 O4QR13 HUMAN	O4QR13 homo sapien

ALIGNMENTS

RESULT 1
HRH4_HUMAN STANDARD, PRT, 390 AA.
ID HRH4_HUMAN
AC O913N8; O9GZ00;
DT 16-OCT-2001 (Ref. 40, Created)
DT 16-OCT-2001 (Ref. 40, Last sequence update)
DT 10-MAY-2005 (Ref. 47, Last annotation update)
DE Histamine H4 receptor (HHR) (GPRV53) (G-protein coupled receptor 105) (GPCR105) (SP9144) (AXOR35).
GN Name=HRH4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Eumarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20538417; PubMed=10973974; DOI=10.1074/jbc.M006480200;
RA Oda T., Morikawa N., Saio Y., Masuno Y., Matsunoto S.-I.;
RT "Molecular cloning and characterization of a novel type of histamine receptor preferentially expressed in leukocytes.";
RL J. Biol. Chem. 275:36781-36786(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE, AND CHARACTERIZATION.
RX TISSUE=Leukocyte; PubMed=11118334; DOI=10.1006/dbrc.2000.4008;
RA Nakamura T., Itadani H., Hidaka Y., Ohta M., Tanaka K.;
RT "Molecular cloning and characterization of a new human histamine receptor, HHR.";
RL Biochem. Biophys. Res. Commun. 279:615-620(2000).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX Jones P.G., Wu S., Betty M.;
RT "Cloning of a novel histamine receptor.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE, AND CHARACTERIZATION.
RX TISSUE=Bone marrow;
RA Liu C., Ma X.-J., Jiang X., Wilson S.J., Hofstra C.L., Blevitt J., Prati J., Li X., Chai W., Garruthers N., Lovenberg T.W.;
RT "Cloning and pharmacological characterization of a fourth histamine receptor (H4) expressed in bone marrow.";
RL Mol. Pharmacol. 59:420-426(2001).
RN [5]
RP NUCLEOTIDE SEQUENCE, AND CHARACTERIZATION.
RX MEDLINE=21104636; PubMed=11181941;
RA Morse K.L., Behan J., Laz T.M., West R.E. Jr., Greenfeder S.A., Anthes J.C., Umhand S., Wan Y., Hipkin K.W., Gonioret W., Shin N., Gustafson E.L., Qiao X., Wang S., Hedrick J.A., Greene J., Bayne M., Monsma F.J. Jr.;
RT "Cloning and characterization of a novel human histamine receptor.";
RL J. Pharmacol. Exp. Ther. 296:1058-1066(2001).

[6]
 RN NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21106320; PubMed=11179436;
 RA Zhu Y., Michalovich D., Wu H.-L., Tan K.B., Dycko G.M., Mannan I.J.,
 RA Boyce R., Alston J., Tierney L.A., Li X., Herrity N.C., Vawter L.,
 RA Sarau H.M., Ames R.S., Davenport C.M., Hieble P., Wilson S.,
 RA Bergama D.J., Fitzgerald L.R.;
 RT "Cloning, expression, and pharmacological characterization of a novel
 RT human histamine receptor."
 RL Mol. Pharmacol. 59:434-441(2001).
 RN [7]
 RN NUCLEOTIDE SEQUENCE.
 RA O'Reilly M.A.;
 RT "Identification of a histamine H4 receptor on human eosinophils - Role
 RT in eosinophil chemotaxis."
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RN NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA).
 RA Publ H.L. Iii, Ikeda S.R., Aronstam R.S.;
 RT "cDNA clones of human proteins involved in signal transduction
 RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: The H4 subclass of histamine receptors could mediate the
 CC histamine signals in peripheral tissues. Displays a significant
 CC level of constitutive activity (spontaneous activity in the
 CC absence of agonist).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Expressed primarily in the bone marrow and
 CC eosinophils. Shows preferential distribution in cells of
 CC immunological relevance such as T-cells, dendritic cells,
 CC monocytes, mast cells, neutrophils. Also expressed in a wide
 CC variety of peripheral tissues, including the heart, kidney, liver,
 CC lung, pancreas, skeletal muscle, prostate, small intestine,
 CC spleen, fetal liver and lymph node.
 CC -1- INDUCTION: Expression is either up-regulated or down-regulated
 CC upon activation of the lymphoid tissues and this regulation may
 CC depend on the presence of IL-10 or IL-13.
 CC -1- MISCELLANEOUS: Does not bind diphenhydramine, loratadine,
 CC ranitidine, cimetidine and chlorpheniramine. Shows modest affinity
 CC for dimaprit, impromidine, clobenpropit, thiooperamide, burinamide
 CC clozapine, imiprepit and imetit. The order of inhibitory activity
 CC was imetit > clobenpropit > burinamide > thiooperamide.
 CC Clobenpropit behaves as a partial agonist, dimaprit and
 CC impromidine show some agonist activity while clozapine behaves as
 CC a full agonist. Thiooperamide shows inverse agonism (enhances cAMP
 CC activity). The order of inhibitory activity of histamine
 CC derivatives was Histamine > N-alpha-methylhistamine > R(-)-alpha-
 CC methylhistamine > S(+)-alpha-methylhistamine. Both N-alpha-
 CC methylhistamine > R(-)-alpha-methylhistamine behave as full
 CC agonists.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

DR InterPro: IPR008102; HistamineRecept_H4.
 DR PANTHER: PTHR19266:SF02; HistamineRecept_H4; 1.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHHODPSN.
 DR PRINTS: PR01726; HISTAMINSHAR.
 DR PROSITE: PS00237; G PROTEIN RECEPT_F1_1; 1.
 DR PROSITE: PS0262; G PROTEIN RECEPT_F2_1; 1.
 DR G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;
 KW Receptor; Transducer; Transmembrane.
 FT TOPO_DOM 1 19
 FT TRANSHEM 20 40
 FT TOPO_DOM 41 52
 FT TRANSHEM 53 73
 FT TOPO_DOM 74 87
 FT TRANSHEM 88 108
 FT TOPO_DOM 109 131
 FT TRANSHEM 132 152
 FT TOPO_DOM 153 172
 FT TRANSHEM 173 193
 FT TOPO_DOM 194 304
 FT TRANSHEM 305 325
 FT TOPO_DOM 326 341
 FT TRANSHEM 342 362
 FT TOPO_DOM 363 390
 FT LIPID 374 374
 FT CARBOHYD 5 5
 FT CARBOHYD 9 9
 FT DISULFID 87 164
 FT CONFLICT 138 138
 FT CONFLICT 206 206
 FT CONFLICT 253 253
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 Best Local Similarity 100.0%; Pred. No. 1.3e-135;
 Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPDNTNINISLSTRVTLAFPMISLVAFIMLGNAVLTLAFVVDNLRHRSYFFLNLAIS 60
 DB 1 MPDNTNINISLSTRVTLAFPMISLVAFIMLGNAVLTLAFVVDNLRHRSYFFLNLAIS 60
 QY 61 DFFGVGISIPLYIPHTLFFMDFGKEICVFWLTDTYLLCTASVYNIIVLISYDRYLSVSNV 120
 DB 61 DFFGVGISIPLYIPHTLFFMDFGKEICVFWLTDTYLLCTASVYNIIVLISYDRYLSVSNV 120
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 DB 121 SYRTQHTGVAKIYTLVAVAVLAFVNGPMILVSESKDESGSECEPFPSEWYTLAITSF 180
 QY 121 SYRTQHTGVAKIYTLVAVAVLAFVNGPMILVSESKDESGSECEPFPSEWYTLAITSF 180
 DB 121 SYRTQHTGVAKIYTLVAVAVLAFVNGPMILVSESKDESGSECEPFPSEWYTLAITSF 180
 QY 181 LEFVPIYILVAFPMNIYNSLMKRDHLSRCQSHGLAVASNTCGHSFRGLSRRSLA 240
 DB 181 LEFVPIYILVAFPMNIYNSLMKRDHLSRCQSHGLAVASNTCGHSFRGLSRRSLA 240
 QY 181 LEFVPIYILVAFPMNIYNSLMKRDHLSRCQSHGLAVASNTCGHSFRGLSRRSLA 240
 DB 181 LEFVPIYILVAFPMNIYNSLMKRDHLSRCQSHGLAVASNTCGHSFRGLSRRSLA 240
 QY 241 STEVPASFSEHORRKSLSLFSSRTKNSNTIASKMSFQSDSVLALHOREHYELLRRR 300
 DB 241 STEVPASFSEHORRKSLSLFSSRTKNSNTIASKMSFQSDSVLALHOREHYELLRRR 300
 QY 241 STEVPASFSEHORRKSLSLFSSRTKNSNTIASKMSFQSDSVLALHOREHYELLRRR 300
 DB 241 STEVPASFSEHORRKSLSLFSSRTKNSNTIASKMSFQSDSVLALHOREHYELLRRR 300
 QY 301 LAKSALILGVPAVCAPYSILFTIVLSFYSSATGPKSVWYRIAFWLQFNSFVNPLLYPL 360
 DB 301 LAKSALILGVPAVCAPYSILFTIVLSFYSSATGPKSVWYRIAFWLQFNSFVNPLLYPL 360
 QY 301 LAKSALILGVPAVCAPYSILFTIVLSFYSSATGPKSVWYRIAFWLQFNSFVNPLLYPL 360
 DB 301 LAKSALILGVPAVCAPYSILFTIVLSFYSSATGPKSVWYRIAFWLQFNSFVNPLLYPL 360
 QY 361 CHKRFQAFPLKIPKIKQPLPSQHSRSVSS 390
 DB 361 CHKRFQAFPLKIPKIKQPLPSQHSRSVSS 390
 RESULT 2
 Q4G016_HUMAN
 ID Q4G016_HUMAN PRELIMINARY; PRT; 390 AA.
 AC Q4G016;
 DT 13-SEP-2005 (TRMBLrel. 31, Created)
 DT 13-SEP-2005 (TRMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TRMBLrel. 31, Last annotation update)

DE Histamine H4 receptor.
 GN Name=HRH4;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 NCBI_TaxID=9606;
 [1]
 RN NUCLEOTIDE SEQUENCE.
 RP TISSUE=Synthetic constructs;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner N., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 Diatchenko L., Marzina K., Farmer A.A., Rubin G.M., Hong L.,
 Stepien M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Ugin T.B., Toshiyuki S., Carninci P., Prange C.,
 Baha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 Blakesley A.C., Kirylenko M.I., Skalska M., Smallus D.E.,
 Butcherfield Y.S.N., Kirylenko M.I., Skalska M., Smallus D.E.,
 RA Schneider A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Synthetic constructs;
 RG NIH NCI Project;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC069136; AAH69136.1; -. mRNA.
 KM Receptor.
 SQ SEQUENCE 390 AA; 44496 MW; C9868BAE7FF912C3 CRC64;
 Query Match 100.0%; Score 2024; DB 2; Length 390;
 Best Local Similarity 100.0%; Pred. No. 1.3e-135;
 Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
 ID 096LD9 HUMAN PRELIMINARY; PRT; 390 AA.
 AC 096LD9;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Histamine receptor H4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 NCBI_TaxID=9606;
 [1]
 RN NUCLEOTIDE SEQUENCE.
 RP TISSUE=Synthetic constructs;
 RC MEDLINE=21106319; PubMed=11179435;
 RA Nguyen T., Shapiro D.A., George S.R., Setola V., Lee D.K., Cheng R.,
 Rausen L., Lee S.P., Lynch K.R., Roth B.L., O'Dowd B.P.;
 RT "Discovery of a novel member of the histamine receptor family."
 RL Mol. Pharmacol. 59:427-433 (2001)
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 DR EMBL: AY008280; AAL09297.1; -. mRNA.
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0004872; F:receptor activity; IEA.
 DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO: GO:0007186; P:G-protein coupled receptor protein signaling. . .; IEA.
 DR GO: GO:0007165; P:signal transduction; IEA.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR InterPro: IPR008102; Histamine_recept_H4.
 DR PANTHER: PTHR19266; SP82; Histamine_recept_H4; 1.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PRO0237; GPCR_RHODOPSN.
 DR PRINTS: PRO1726; HISTAMINEH4R.
 DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: PS0262; G_PROTEIN_RECEP_F2_1; 1.
 KM G-protein coupled receptor; Receptor; Transducer; Transmembrane.
 SQ SEQUENCE 390 AA; 44470 MW; CC8285D30D216C66 CRC64;
 Query Match 99.6%; Score 2016; DB 2; Length 390;
 Best Local Similarity 99.7%; Pred. No. 4.9e-135;
 Matches 389; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 4

Q8MNV9_PIG PRELIMINARY; PRT; 390 AA.

AC Q8MNV9; DT 01-MAR-2002 (TReMBLrel. 20, Created)

DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)

DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)

DE Histamine H4 receptor.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae;

OC Sus.

NCBI_TaxID=96823;

RN Nucleotide sequence.

RC TISSUE=Spleen;

RX MEDLINE=22015261; PubMed=12020829; DOI=10.1016/S0167-4781(02)00236-1;

RA Oda T., Matsumoto S., Masuko Y., Takasaki J., Matsumoto M.,

RA Kamohara M., Saito T., Ohishi T., Soga T., Hiyma H., Matsushima H.,

RA Furuchi K.;

RT "CDNA cloning and characterization of porcine histamine H4 receptor,"

RL Blochim. Biophys. Acta 1575:135-138 (2002)

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

DR EMBL; AB053300; BAB93078.1; -; mRNA.

DR GO; GO:0016021; C:Integral to membrane; IEA.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0007184; F:rhodopsin-like receptor activity; IEA.

DR GO; GO:0007185; P:signal transduction; IEA.

DR InterPro; IPR000276; GPCR_Rhodopsn.

DR PANTHER; PTHR19266:SF82; Histamine_recept_H4; 1.

DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PR00237; GPCRHOPOPSN.

DR PRINTS; PR01726; HISTAMINEH4R.

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

DR G-protein coupled receptor; Receptor; Transducer; Transmembrane.

KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.

SEQUENCE 390 AA; 44483 MW; BC6FD363A6F4D3F CRC64;

Query Match 71.0%; Score 1436.5; DB 2; Length 390;

Best Local Similarity 72.9%; Pred. No. 6.7e-94;

Matches 283; Conservative 30; Mismatches 72; Indels 3; Gaps 3;

QY 3 DTNSTINISLSTRVTLAFMSLVAFAMIGNALVTLAFVVDKNLRHRSYFFFLNLAISDF 62

DB 6 DTN-TNTPLETRIALAFMSLVAFAMIGNALVTLAFVVDKNLRHRSYFFFLNLAISDF 64

QY 63 FVGVISIPLYIPHTLFEMDFGKEICVFWLTDDYLLCTASVYINVLISYDRYLSVSNVAV 122

DB 65 FVGVISIPLYIPHTLFEMDFGKEICVFWLTDDYLLCTASVYINVLISYDRYLSVSNVAV 124

QY 123 RTQHTGVAKITVLAFAVAVVLAFLVNGPMILVSESKDGSCECPFESEVTLAITSLE 182

DB 125 RTQHTGVAKITVLAFAVAVVLAFLVNGPMILVSESKDGSCECPFESEVTLAITSLE 184

QY 183 FVIVITVLAFAVAVVLAFLVNGPMILVSESKDGSCECPFESEVTLAITSLE 242

DB 185 FVIVITVLAFAVAVVLAFLVNGPMILVSESKDGSCECPFESEVTLAITSLE 244

QY 243 EVPAFSHSEORRKSLSMFSRTKNSNTIASKMGFSQSDSVLAHQREHVELLRARLA 302

DB 245 EVPAFSHSEORRKSLSMFSRTKNSNTIASKMGFSQSDSVLAHQREHVELLRARLA 303

QY 303 KSLAILLGAVFAVAVVLAFLVNGPMILVSESKDGSCECPFESEVTLAITSLE 362

DB 304 KSLAILLGAVFAVAVVLAFLVNGPMILVSESKDGSCECPFESEVTLAITSLE 363

QY 363 KRFQKAFIKICIKOPLPSOHSRSVSS 390

DB 364 KRFQKAFIKICIKOPLPSOHSRSVSS 390

RESULT 5 Q91ZY1_RAT PRELIMINARY; PRT; 391 AA.

AC Q91ZY1; DT 01-DEC-2001 (TReMBLrel. 19, Created)

DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)

DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)

DE Histamine H4 receptor.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Rattus.

OC NCBI_TaxID=10116;

RN Nucleotide sequence.

RC STRAIN=Sprague-Dawley;

RA Liu C., Wilson S., Kuel C., Lovenberg T.W.;

RL Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

DR EMBL; AF358860; AAK97381.1; -; mRNA.

DR EMBL; ENSRN00000016887; Rattus norvegicus.

DR RGD; 620631; Hrh4.

DR GO; GO:0016021; C:Integral to membrane; IEA.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0007184; F:rhodopsin-like receptor activity; IEA.

DR GO; GO:0007185; P:signal transduction; IEA.

DR InterPro; IPR000276; GPCR_Rhodopsn.

DR PANTHER; PTHR19266:SF82; Histamine_recept_H4; 1.

DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PR00237; GPCRHOPOPSN.

DR PRINTS; PR01726; HISTAMINEH4R.

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

DR G-protein coupled receptor; Receptor; Transducer; Transmembrane.

KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.

SEQUENCE 391 AA; 44023 MW; C707BA6E339CFED41 CRC64;

Query Match 69.8%; Score 1413.5; DB 2; Length 391;

Best Local Similarity 69.4%; Pred. No. 2.3e-92;

Matches 272; Conservative 40; Mismatches 77; Indels 3; Gaps 2;

QY 1 MPDTNSTINISLSTRVTLAFMSLVAFAMIGNALVTLAFVVDKNLRHRSYFFFLNLAIS 60

DB 1 MDSNGTDVLPTRQVPLAFMSLVAFAMIGNALVTLAFVVDKNLRHRSYFFFLNLAIS 60

QY 61 DFFVGVISIPLYIPHTLFEMDFGKEICVFWLTDDYLLCTASVYINVLISYDRYLSVSNV 120

DB 61 DFFVGVISIPLYIPHTLFEMDFGKEICVFWLTDDYLLCTASVYINVLISYDRYLSVSNV 120

QY 121 SYRQHTGVAKITVLAFAVAVVLAFLVNGPMILVSESKDGS--ECBPGFESEVTLAITS 178

DB 121 SYRQHTGVAKITVLAFAVAVVLAFLVNGPMILVSESKDGS--ECBPGFESEVTLAITS 180

QY 179 SFLEFVPLVLAFAVAVVLAFLVNGPMILVSESKDGS--ECBPGFESEVTLAITS 238

DB 181 SFLEFVPLVLAFAVAVVLAFLVNGPMILVSESKDGS--ECBPGFESEVTLAITS 240

QY 239 SASTEVPAFSHSEORRKSLSMFSRTKNSNTIASKMGFSQSDSVLAHQREHVELLRARLA 298

DB 241 SASTEVPAFSHSEORRKSLSMFSRTKNSNTIASKMGFSQSDSVLAHQREHVELLRARLA 300

QY 299 KRLAKSLAILLGAVFAVAVVLAFLVNGPMILVSESKDGS--ECBPGFESEVTLAITS 358

DB 301 KRLAKSLAILLGAVFAVAVVLAFLVNGPMILVSESKDGS--ECBPGFESEVTLAITS 360

QY 359 PLCHKRFQKAFIKICIKOPLPSOHSRSVSS 390

Db 361 PLCHRRFOKAFMKILCTKOPASQ-TQSVSS 391

RESULT 6

091ZY2 MOUSE
ID 091ZY2 MOUSE PRELIMINARY; PRT; 391 AA.
AC 091ZY2;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Histamine H4 receptor.
GN Name=H4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALE/c;
RA Liu C., Wilson S., Kuei C., Lovenberg T.W.;
RL Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR EMBL; AF358859; AAK7380.1; -; mRNA.
DR Ensembl; ENSMUSG0000037346; Mus musculus.
DR MGI; MGI:2429635; H4.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005887; C:integral to plasma membrane; IC.
DR GO; GO:0005624; C:membrane fraction; IDA.
DR GO; GO:0004969; F:histamine receptor activity; IDA.
DR GO; GO:0006954; P:inflammatory response; TAS.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR008102; Histamine_recept_H4.
DR PANTHER; PTHR19266; SF82; Histamine_recept_H4; 1.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PRINTS; PR01726; HISTAMINEH4.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 391 AA; 44249 MW; 59BC73CB5214C5E0 CRC64;

Query Match Best Local Similarity 68.1%; Score 1377.5; DB 2; Length 391;
Matches 268; Conservative 40; Mismatches 81; Indels 3; Gaps 2;

QY 1 MPDINSLTSLSTRVTLAFMSLVAFAIMGNALVTLAFVVDKRLRRSSYFLNLAIIS 60
DB 1 MSENSTGTLPLPAQVPLAFMSLFAIMGNNAVTLAFVVDRLRRSNYPFLNLAIIS 60
QY 61 DFFGVGISIPLYIHTLEPMDFGKEICVFMLTDTLLCTASVYNIIVLISYRYISVSNV 120
DB 61 DFLVGLSISIPLYIHTLEPMDFGKEICVFMLTDTLLCTASVYNIIVLISYRYISVSNV 120
QY 121 SYRTQHTGVLTIVTLAVVAVTLAVNGPMILVSESWKDEGS--ECEBGFSEWYIIAIT 178
DB 121 SYRQHTGIMKIVIAQVAVVAVTLAVNGPMILVSESWKDEGS--ECEBGFSEWYIIAIT 180
QY 179 SFLFVLPVILVAVFNNMTIYSLMKRDLSCQSHPGILTAVSSNICGHSFGRGLSSRSL 238
DB 181 MLLEFLPVLISVAVFNNMTIYSLMKRDLSCQSHPGILTAVSSNICGHSFGRGLSSRSL 240
QY 239 SASTVEPASPFSEBORRKSLSMFSRTGNSNTIASKWSFSQSDSVLAHQREHVELLRA 298
DB 241 PGLKESASRSESBRKRSILVSLRTMNSITLAFKGSFWRSESAALRREVAELLRG 300
QY 299 RRLAKSLAIIILGVAVCAVPSLFTIVLSFYSSATGPKSVYRIAFMLQWENSFVNPLY 358
DB 301 RKLARSLAIIILSAFAICVAPYCLFTIVLSTYPRTERPKSVYRIAFMLQWENSFVNPLY 360
QY 359 PLCHRRFOKAFMKILCTKOPASQ-TQSVSS 390

Db 361 PLCHRRFOKAFMKILCTKOPALSQ-NQSVSS 391

RESULT 7

091ZY3 CAVPO
ID 091ZY3 CAVPO PRELIMINARY; PRT; 389 AA.
AC 091ZY3;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Histamine H4 receptor.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC Hystricognathi; Caviidae; Cavia.
OX NCBI_Taxid=10141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Liu C., Wilson S., Kuei C., Lovenberg T.W.;
RL Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR EMBL; AF358858; AAK7379.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR008102; Histamine_recept_H4.
DR PANTHER; PTHR19266; SF82; Histamine_recept_H4; 1.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PRINTS; PR01726; HISTAMINEH4.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 389 AA; 44512 MW; 51AF32FD6F7C3B4F CRC64;

Query Match Best Local Similarity 65.1%; Score 1318.5; DB 2; Length 389;
Matches 253; Conservative 48; Mismatches 83; Indels 3; Gaps 3;

QY 5 NSTINLSLSTRVTLAFMSLVAFAIMGNALVTLAFVVDKRLRRSSYFLNLAIISDFEV 64
DB 5 NSTIALT-SIKISLTFLMSLAIAMGNVAVTLAFVVDENLRHSNYPFLNLAIADFFV 63
QY 65 GVISIPLYIHTLEPMDFGKEICVFMLTDTLLCTASVYNIIVLISYRYISVSNVYRT 124
DB 64 GAIAIPLYIPSSLTLYWSGKQACVFMLTDTLLCTASVYNIIVLISYRYISVSNVYRA 123
QY 125 QHTGVLTIVTLAVVAVTLAVNGPMILVSESWKDEGSCEPGEFSEWYIIAITSFLEFV 184
DB 124 QHSGTWKLTIAQVAVVAVTLAVNGPMILVSESWKDEGSCEPGEFSEWYIIAITSFLEFV 183
QY 185 IPVLVAVFNNMTIYSLMKRDLSCQSHPGILTA-VSSNICGHSFGRGLSSRSLASTE 243
DB 184 IPIVLVAVFNNMTIYSLMKRDLSCQSHPGILTA-VSSNICGHSFGRGLSSRSLASTE 243
QY 244 VPASFSERORRKSLSMFSRTGNSNTIASKWSFSQSDSVLAHQREHVELLRA 303
DB 244 TYSAGSDKSRKRSLSMFSRTGNSNTIASKWSFSQSDSVLAHQREHVELLRA 303
QY 304 SLAIIILGVAVCAVPSLFTIVLSFYSSATGPKSVYRIAFMLQWENSFVNPLYPLCHK 363
DB 304 SLAIIILGVAVCAVPSLFTIVLSFYSSATGPKSVYRIAFMLQWENSFVNPLYPLCHK 363
QY 364 RFOKAFMKILCTKOPALSQ-NQSVSS 390
DB 364 RFOKAFMKILCTKOPALSQ-NQSVSS 389

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RESULT 8
Q69J5_PANTR
ID Q69J5_PANTR PRELIMINARY; PRT; 175 AA.
AC Q69J5;
DT 05-JUL-2004 (TREMblrel. 27, Created)
DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
DE Histamine receptor H4 subtype (Fragment).
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Pan.
NCBI_TaxID=9598;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15123584; DOI=10.1101/gr.1891104;
RA Zhang J., Wang X., Podlaha O.;
RT "Testing the chromosomal speciation hypothesis for humans and
chimpanzees."; 14:845-851(2004).
RL Genome Res. 14:845-851(2004).
DR EMBL; AY561469; AAT45507.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR PANTHER; PTHR19266:SF82; Histaminrecept_H4; 1.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PRINTS; PR01726; HISTAMINEH4R.
DR PROSITE; PS50262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
FT NON_TER 1
FT TER 175
SQ SEQUENCE 175 AA; 19825 MW; E5961PDAC315182F CRC64;

Query Match 43.9%; Score 889; DB 2; Length 175;
Best Local Similarity 97.7%; Pred. No. 2,1e-55;
Matches 171; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 206 HLRCSQHPGLTAVSSNICGHSFRGLSSRRSLASSTVEVPASFSERORRKSILMFSSRT 265
DB 1 HLRCSQHPGLTAVSSNICGHSFRGLSSRRSLASSTVEVPASFSERORRKSILMFSSRT 60
QY 266 KMSNNTIAAKKGSFSDSDVALHOREHVELLRARLAKSLAILLGVPVCAWAPYSLEFTIV 325
DB 61 KMSNNTIAAKKGSFSDSDVALHOREHVELLRARLAKSLAILLGVPVCAWAPYSLEFTIV 120
QY 326 LSFYSSTAGPKSVWYRIAFWLGWNSFVNPLLYPLCHKRFOKAFKIFCIKKOP 380
DB 121 LSFYSSTAGPKSVWYRIAFWLGWNSFVNPLLYPLCHKRFOKAFKIFCIKKOP 175

RESULT 9
Q69J34_9PRIM
ID Q69J34_9PRIM PRELIMINARY; PRT; 174 AA.
AC Q69J34;
DT 05-JUL-2004 (TREMblrel. 27, Created)
DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
DE Histamine receptor H4 subtype (Fragment).
OS Gorilla gorilla (Gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Gorilla.
NCBI_TaxID=9593;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15123584; DOI=10.1101/gr.1891104;
RA Zhang J., Wang X., Podlaha O.;

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RT "Testing the chromosomal speciation hypothesis for humans and
chimpanzees."; 14:845-851(2004).
RL Genome Res. 14:845-851(2004).
DR EMBL; AY561470; AAT45508.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR PANTHER; PTHR19266:SF82; Histaminrecept_H4; 1.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PRINTS; PR01726; HISTAMINEH4R.
DR PROSITE; PS50262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
FT NON_TER 1
FT TER 174
SQ SEQUENCE 174 AA; 19713 MW; 4038B74734A785F5 CRC64;

Query Match 43.6%; Score 882; DB 2; Length 174;
Best Local Similarity 97.1%; Pred. No. 6,5e-55;
Matches 169; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 206 HLRCSQHPGLTAVSSNICGHSFRGLSSRRSLASSTVEVPASFSERORRKSILMFSSRT 265
DB 1 HLRCSQHPGLTAVSSNICGHSFRGLSSRRSLASSTVEVPASFSERORRKSILMFSSRT 60
QY 266 KMSNNTIAAKKGSFSDSDVALHOREHVELLRARLAKSLAILLGVPVCAWAPYSLEFTIV 325
DB 61 KMSNNTIAAKKGSFSDSDVALHOREHVELLRARLAKSLAILLGVPVCAWAPYSLEFTIV 120
QY 326 LSFYSSTAGPKSVWYRIAFWLGWNSFVNPLLYPLCHKRFOKAFKIFCIKKOP 379
DB 121 LSFYSSTAGPKSVWYRIAFWLGWNSFVNPLLYPLCHKRFOKAFKIFCIKKOP 174

RESULT 10
Q65E1_MACMU
ID Q65E1_MACMU PRELIMINARY; PRT; 445 AA.
AC Q65E1;
DT 01-JUN-2003 (TREMblrel. 24, Created)
DT 01-JUN-2003 (TREMblrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE Histamine receptor H3.
GN Name=HRH3;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopitheciidae; Cercopitheciinae; Macaca.
NCBI_TaxID=9544;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Yao B.B., Sharma R., Caser S., Espenshade T.A., Hancock A.A.;
Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR EMBL; AY231164; AAO63757.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004899; F:histamine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007186; P:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007165; P:G-protein coupled receptor protein signalin. . .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR003980; H3_receptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PRINTS; PR01471; HISTAMINEH3R.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECP_F1_2; 1.

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	RT	"Cloning of mouse histamine H3 receptor."
	Rt	Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
	CC	-1- FUNCTION: The H3 subclass of histamine receptors could mediate the histamine signals in CNS and peripheral nervous system. Signals through the inhibition of adenylyl cyclase and displays high constitutive activity (spontaneous activity in the absence of agonist) (By similarity).
	CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.
	CC	-1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
	CC	This Swiss-Prot entry is copyrighted. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
	CC	removed.
	DR	EMBL; AY044153; AAK72406.1; -, mRNA.
	DR	Ensembl; ENSMUSG0000039059; Mus musculus.
	DR	MGI; MGI:2139279; Hrh3.
	DR	GO; GO:0016021; C:integral to membrane; TAS.
	DR	InterPro; IPR000276; GPCR_Rhodopn.
	DR	InterPro; IPR003980; H3_receptor.
	DR	Pfam; PF00001; 7tm_1; 1.
	DR	PRINTS; PR00237; GPCRRHODOPSN.
	DR	PRINTS; PR01471; HISTAMINEH3R.
	DR	PROSITE; PS00237; G PROTEIN RECD F1 1; 1.
	DR	PROSITE; PSS0262; G_PROTEIN_RECD_F1_2; 1.
	Kw	G-protein coupled receptor; Glycoteleins; Receptor; Transducer; Transmembrane.
	Kw	TOPO_DOM . 1 39 Extracellular (Potential). Potential.
	FT	TRANSMEM 40 60 Potencial.
	FT	TOPO_DOM 61 70 Cytoplasmic (Potential).
	FT	TRANSEM 71 91 Potencial.
	FT	TOPO_DOM 92 108 Extracellular (Potential).
	FT	TRANSEM 109 129 Potencial.
	FT	TOPO_DOM 130 156 Cytoplasmic (Potential).
	FT	TRANSEM 157 177 Potencial.
	FT	TOPO_DOM 178 196 Extracellular (Potential).
	FT	TRANSEM 197 217 Potencial.
	FT	TOPO_DOM 218 359 Cytoplasmic (Potential).
	FT	TRANSEM 360 380 Potencial.
	FT	TOPO_DOM 381 396 Extracellular (Potential).
	FT	TRANSEM 397 417 Potencial.
	FT	TOPO_DOM 418 445 Cytoplasmic (Potential).
	FT	COMPTAS 20 23 Poly-Aa.
	FT	CABOBYD 11 11 N-linked (GlcNAc...) (Potential).
	SQ	SEQUENCE 445 AA; 48541 MW; B8D406E29E1F3C5F CRC64;
		Query Match 35.9%; Score 72.7; DB 1; Length 445;
		Best Local Similarity 38.8%; Pred. No. 1.8e-43;
		Matches 165; Conservative 54; Mismatches 132; Indels 74; Gaps 10;
Oy	11	SLSTRVTLAFMSIVAFAIMGNALVTIAFPVDKNLRHSYFFLNLAISDFYGVISIP 70
Dd	30	SAATVAITVALMALMLIYAIVTLAGNALWMAFAVASLSLTQNPFLLNLAISPVLGAFCIP 89
Oy	71	LYIPHTLP-EWDGKEKICVFELTTDYILCTRAVSNTYIVLISIDRLYSNANASYTGHTGV 129
Dd	90	LVPYVYLTVGTWTFGRGCKLMLVDDYILCASSVENIYLISTDFLSTRAVSYPAAQGDT 149
Oy	130	LKIYTLVAVAWVLAFLNGMPILVSESK-----DEGECEPGEFSEWYIALITSFL 181
Dd	150	RRARRKALWVWLAFLLXGPAIL---SWETLISGGSSIPBG-HCYAEFYNNYFILITASLT 205
Oy	182	EFLVPIVLIVAYFNNNIY-----WSMKRD 205
Dd	206	EFFPPPLISTVFENLSTYLIQRTRRLDGRAGAPPPPDQAQSPAPPAPSCGWCPKG 265
Oy	206	HLSRCQSH-----PGLTRAVSSNTIGCHSRGLSRRSLSATVEVASHSERORKS 257
Dd	266	HGEAMPPIHRVGVGEGAGVGTEGAGLOGGGSGGGAAPAPTSSGGS-----SKGTGPR 318
Oy	258	SLMFSSSTTKNSNTIASIKMGSSFQSSDSVLHQREHVELLRARIRAKSLAIIILGFVAVCWA 317


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Db      319 SLKGSKSPASASALEKMKVOSIT-----QFRLSRDKKAKSLALIVISIFGLCMA 372
Qy      318 PYSLETTIVLSPYSSATGPKSVWYRIAFMLOWNSFVNPLYPPLCHKRQOKFLKIFC--- 374
Db      373 PYTLIMTIIRACHGHCVP-DVWYETSFMLMANSVAVNPVLYPLCHYSTRRAFTLLCGCK 431
Qy      375 IKKOP 379
Db      432 LKVOP 436

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ID      Q540P3_MOUSE PRELIMINARY; PRT; 445 AA.
AC      Q540P3;
DT      13-SEP-2005 (TREMBlrel. 31, Created)
DT      13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT      13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE      Histamine H3 receptor.
GN      Name=H3h3;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=C57BL/6J; TISSUE=Brain;
RX      MEDLINE=22592891; PubMed=12706455; DOI=10.1016/S0014-2999(03)01635-2;
RA      Chen J., Liu C., Lovenberg T.W.;
RT      "Molecular and pharmacological characterization of the mouse histamine
RT      H(3) receptor.";
RL      Eur. J. Pharmacol. 467:57-65(2003).
CC      -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC      -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR      EMBL; AY142155; AAN34941.1; -; mRNA.
DR      MGI; MGI:2139279; H3h3.
DR      GO; GO:0016021; C:Integral to membrane; TAS.
DR      InterPro; IPR000276; GPCR_Rhodopsn.
DR      InterPro; IPR003980; H3_receptor.
DR      Pfam; PF00001; 7tm.1; 1_receptor.
DR      PRINTS; PR00237; GPCR_RHODOPSN.
DR      PROSITE; PRO1471; HISTAMINEH3R.
DR      PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR      PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR      G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ      SEQUENCE 445 AA; 48541 MW; BBD406E29E1F3CF CRC64;

Query Match 35.9%; Score 727; DB 2; Length 445;
Best Local Similarity 38.8%; Pred. No. 1.8e-43;
Matches 165; Conservative 54; Mismatches 132; Indels 74; Gaps 10;

Db      11 SLSTRVTLAFMSLVAFAMGNLVIAFVVDKRLHRSSYFFPLNTAISDFVGVISIP 70
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Db      30 SAANTAVTALMALGLIYATVYVGNLVIAFVADSLRTQNNFFPLNTAISDFLVGAFICP 89
Qy      71 LYIHTLLE-EMDFGEKICVFWLTDTYLLCTASVYNIIVLISDRYLSVSNASVYRTQHTGV 129
Db      90 LYVYVTLTGRTTFGRGCKLMLVVDYLLCASSVFNIVLISDRFLSVTRAVSYRAQOQDT 149
Qy      130 LKIYTLVAVVAVLAVLVNGPMILVSESK-----DESGECRPGFSEWYIATISFL 181
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Qy      182 EFVLPVILVAVFNNMNY-----WSLWGRD 205
Db      206 EFTFPLSVTFPNIISLYNIQRTRRLLDGAREAGPEPPDAQSPPPAPSCGCMWRG 265
Qy      206 HLSRCQSH-----PGLTAVSNICGHSFPGRLSSRRSLASRETVASFSHSEQRQRKS 257
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Qy      318 PYSLETTIVLSPYSSATGPKSVWYRIAFMLOWNSFVNPLYPPLCHKRQOKFLKIFC--- 374
Db      373 PYTLIMTIIRACHGHCVP-DVWYETSFMLMANSVAVNPVLYPLCHYSTRRAFTLLCGCK 431
Qy      375 IKKOP 379
Db      432 LKVOP 436

RESULT 14
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AC      Q5G535;
DT      10-MAY-2005 (TREMBlrel. 30, Created)
DT      10-MAY-2005 (TREMBlrel. 30, Last sequence update)
DT      10-MAY-2005 (TREMBlrel. 30, Last annotation update)
DE      Histamine H3 receptor long form.
OS      Phodopus sungorus (Striped hairy-footed hamster) (Djungarian hamster).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muridae; Cricetinae; Phodopus.
OX      NCBI_TaxID=10044;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      PubMed=15618354; DOI=10.1210/en.2004-1452;
RA      Barrett P., Rose A.W., Balik A., Littlewood P.A., Mercer J.G.,
RA      Moar K.M., Salminen T., Karlin J., Panula P., Schueller S., Edling F.J.,
RA      Ubeda C., Morgan P.J.;
RT      "Photoperiodic Regulation of Histamine H3 Receptor and VGF Messenger
RT      Ribonucleic Acid in the Arcuate Nucleus of the Siberian Hamster.";
RL      Endocrinology 146:1930-1939(2005).
CC      -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC      -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR      EMBL; AY855070; AAM57886.1; -; mRNA.
DR      GO; GO:0016021; C:Integral to membrane; IEA.
DR      GO; GO:0004969; F:histamine receptor activity; IEA.
DR      GO; GO:0004872; F:receptor activity; IEA.
DR      GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR      GO; GO:0007186; P:G-protein coupled receptor protein signaln. . .; IEA.
DR      GO; GO:0007165; P:signal transduction; IEA.
DR      InterPro; IPR000276; GPCR_Rhodopsn.
DR      InterPro; IPR003980; H3_receptor.
DR      Pfam; PF00001; 7tm.1; 1_receptor.
DR      PRINTS; PR00237; GPCR_RHODOPSN.
DR      PROSITE; PRO1471; HISTAMINEH3R.
DR      PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR      PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR      G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ      SEQUENCE 445 AA; 48488 MW; DD8969E9D192BF22 CRC64;

Query Match 35.9%; Score 727; DB 2; Length 445;
Best Local Similarity 39.3%; Pred. No. 1.8e-43;
Matches 167; Conservative 51; Mismatches 133; Indels 74; Gaps 10;

Db      11 SLSTRVTLAFMSLVAFAMGNLVIAFVVDKRLHRSSYFFPLNTAISDFVGVISIP 70
Qy      11 SLSTRVTLAFMSLVAFAMGNLVIAFVVDKRLHRSSYFFPLNTAISDFVGVISIP 70
Db      30 SAANTAVTALMALGLIYATVYVGNLVIAFVADSLRTQNNFFPLNTAISDFLVGAFICP 89
Qy      71 LYIHTLLE-EMDFGEKICVFWLTDTYLLCTASVYNIIVLISDRYLSVSNASVYRTQHTGV 129
Db      90 LYVYVTLTGRTTFGRGCKLMLVVDYLLCASSVFNIVLISDRFLSVTRAVSYRAQOQDT 149
Qy      130 LKIYTLVAVVAVLAVLVNGPMILVSESK-----DESGECRPGFSEWYIATISFL 181
Db      150 RRAVRKALVAVLAVLVNGPMILVSESK-----SWEYLSGSSSIPEG-HCYAEFFYNYFLITASTL 205
Qy      182 EFVLPVILVAVFNNMNY-----WSLWGRD 205
Db      206 EFTFPLSVTFPNIISLYNIQRTRRLLDGAREAGPEPPDAQSPPPAPSCGCMWRG 265
Qy      206 HLSRCQSH-----PGLTAVSNICGHSFPGRLSSRRSLASRETVASFSHSEQRQRKS 257
Db      266 HGEAMPILHYVGAVGEGVGEAGLGGSGGGAASFTSSSGSS-----SRQTEPR 318

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OM protein - protein search, using sw model

Run on: March 28, 2006, 13:58:45 ; Search time 48 Seconds
(without alignments)
671.740 Million cell updates/sec

Title: US-10-616-088-2

Perfect score: 2024
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Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents AA:*
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6: /cgn2_6/ptodata/1/iaa/backfill1est.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2024	100.0	390	2	US-09-414-010-2
2	2024	100.0	390	2	US-09-812-216-2
3	2024	100.0	390	2	US-09-875-076-14
4	730	36.1	445	2	US-10-453-106-2
5	729	36.0	445	2	US-09-165-543-5
6	729	36.0	445	2	US-09-891-053-25
7	729	36.0	445	2	US-10-453-106-3
8	724	35.8	445	1	US-08-985-090-2
9	724	35.8	445	2	US-09-165-543-2
10	724	35.8	445	2	US-09-167-354-7
11	724	35.8	445	2	US-09-642-855-7
12	724	35.8	445	2	US-09-642-854-7
13	724	35.8	445	2	US-09-642-852-7
14	724	35.8	445	2	US-10-453-106-1
15	724	35.8	445	2	US-09-949-016-10930
16	724	35.8	453	2	US-09-891-053-20
17	722	35.7	413	2	US-09-891-053-1
18	632	31.2	351	2	US-09-524-162-2
19	593	29.3	362	1	US-08-985-090-5
20	593	29.3	362	2	US-09-165-543-32
21	434.5	21.5	355	1	US-08-118-270-11
22	434.5	21.5	355	4	PCT-US93-08528-11
23	416	20.6	348	1	US-08-118-270-13
24	416	20.6	348	4	PCT-US93-08528-13
25	411	20.3	590	2	US-09-538-092-967
26	406	20.1	590	2	US-09-826-509-517
27	405.5	20.0	515	2	US-09-688-415-10

28	402.5	19.9	513	1	US-08-406-855A-21	Sequence 21, Appl
29	402.5	19.9	513	2	US-09-206-899-21	Sequence 21, Appl
30	402.5	19.9	515	1	US-08-444-734A-7	Sequence 7, Appl
31	402.5	19.9	515	1	US-08-406-855A-22	Sequence 22, Appl
32	402.5	19.9	515	2	US-09-206-899-22	Sequence 22, Appl
33	400.5	19.8	515	1	US-08-722-001-25	Sequence 25, Appl
34	400.5	19.8	515	2	US-09-688-415-9	Sequence 9, Appl
35	399.5	19.7	517	1	US-08-467-568-10	Sequence 10, Appl
36	399.5	19.7	517	1	US-09-030-582-10	Sequence 10, Appl
37	399.5	19.7	520	1	US-08-334-698-4	Sequence 4, Appl
38	399.5	19.7	520	1	US-08-228-932-4	Sequence 4, Appl
39	399.5	19.7	520	1	US-08-468-939-4	Sequence 4, Appl
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41	399.5	19.7	520	1	US-08-722-190-4	Sequence 4, Appl
42	399.5	19.7	520	2	US-08-244-354-4	Sequence 4, Appl
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ALIGNMENTS

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RESULT 1
US-09-414-010-2
; Sequence 2, Application US/09414010
; Patent No. 6204017
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Iaz, Thomas M.
; APPLICANT: Morzema, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/414, 010
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-414-010-2
Query Match 100.0%; Score 2024; DB 2; Length 390;
Best Local Similarity 100.0%; Pred. No. 1.1e-159;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPDNTNINSLSTRVTLAFMSLVAFAIMGNALVTLAFVDKRLRHRSYFFLNLAIS 60
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DB 61 DFVGVGISILYIPHTLFEWDPKKEICVFWLTDYLLCTASVNYILISYDRILSVNAV 120
61 DFVGVGISILYIPHTLFEWDPKKEICVFWLTDYLLCTASVNYILISYDRILSVNAV 120
QY 121 SYRTQHTGVKLTWLVAVVLAFLVNGPMILVSESMKDGSCDCEPFESEWYLLATTSF 180
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DB 181 LEFVPIVILVAYFNNMIYWSLWTRDHLSCROSHPLGLTAVSSNICGHSFRGLSSRSLA 240
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241 STEVPASFSERRRKSSLSMFSRTGNSVTISLKKGSFQSSVALHOREHVELLARR 300
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RESULT 2

US-09-812-216-2
Sequence 2, Application US/09812216
Patent No. 661353
GENERAL INFORMATION:
APPLICANT: Behan, Jjiang Xu
APPLICANT: Hedrick, Joseph A.
APPLICANT: Laz, Thomas M.
APPLICANT: Monsma, Frederick J. Jr.
APPLICANT: Morse, Kelley L.
APPLICANT: Umland, Shelby P.
APPLICANT: Wang, Suke
TITLE OF INVENTION: Histamine receptor
FILE REFERENCE: CN01069
CURRENT APPLICATION NUMBER: US/09/812,216
CURRENT FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 09/414,010
PRIOR FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 390
TYPE: PRT
ORGANISM: Homo sapiens
US-09-812-216-2

Query Match 100.0%; Score 2024; DB 2; Length 390;
Best Local Similarity 100.0%; Pred. No. 1,1e-159;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3

US-09-875-076-14
Sequence 14, Application US/09875076
Patent No. 6869776
GENERAL INFORMATION:
APPLICANT: Chen, Ruoping
APPLICANT: Dang, Huong T.

APPLICANT: Liaw, Chen W.
APPLICANT: Lin, I-Ilin
TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
FILE REFERENCE: AREN0050
CURRENT APPLICATION NUMBER: US/09/875,076
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 09/417,044
PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR FILING DATE: 1999-02-16
PRIOR APPLICATION NUMBER: 60/121,851
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/123,946
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,949
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/136,436
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,437
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PRIOR FILING DATE: 1999-05-28
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PRIOR FILING DATE: 1999-06-29
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PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/156,634
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/157,280
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,294
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,281
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,293
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,282
PRIOR FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 390
TYPE: PRT
ORGANISM: Homo sapiens
US-09-875-076-14

Query Match 100.0%; Score 2024; DB 2; Length 390;
Best Local Similarity 100.0%; Pred. No. 1,1e-159;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPDNTSTINISLSTRVTLAFPMSLVAFPAIMLGNALVILAFVVDKQNRHRSYFFLNLAIS 60
Db 1 MPDNTSTINISLSTRVTLAFPMSLVAFPAIMLGNALVILAFVVDKQNRHRSYFFLNLAIS 60
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Db 61 DFEVGVISIPLYIPHTLFEMDFGKEICVFMLTTDYLLCTASVYNIYLISYDRYLSVSNAY 120
QY 121 SYRTQHTGVKIVTLMAVAVWLAFVNGPMILVSESMKDESGCEPGFSEMYLLAITSF 180
Db 121 SYRTQHTGVKIVTLMAVAVWLAFVNGPMILVSESMKDESGCEPGFSEMYLLAITSF 180
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Db 301 LAKSLATLLGVPAVCAWAPYSFTYLSFYSSTAGKSWYRIAPLQWNSFVNPL 360
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RESULT 4
US-10-453-106-2
; Sequence 2, Application US/10453106
; Patent No. 6906060
; GENERAL INFORMATION:
; APPLICANT: Peschke, Bernd
; APPLICANT: Hohweg, Rolf
; TITLE OF INVENTION: SUBSTITUTED HEXAHYDROPYRROLO[1,2-a]PYRAZINES,
; TITLE OF INVENTION: OCTAHYDROPYRROLO[1,2-a]PYRAZINES AND
; TITLE OF INVENTION: DECAHYDROPYRAZINO[1,2-a]AZEPINES
; FILE REFERENCE: 6483.200-US
; CURRENT APPLICATION NUMBER: US/10/453,106
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: US 60/387,047
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: Danish Application no. PA 2002 00863
; PRIOR FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 2
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Monkey
US-10-453-106-2

Query Match 36.1%; Score 730; DB 2; Length 445;
Best Local Similarity 39.2%; Pred. No. 1.7e-52;
Matches 168; Conservative 47; Mismatches 132; Indels 82; Gaps 10;

Qy 11 SLSTRVTTLAFMSIVAFAMIGNALVILAFVVDKMLRRSSYFFLNLAISDFVGVISIP 70
Db 30 SAATTAVALAAMALLIVATVIGNALVILAFVADSLSRTQNNFFLNLAISDFVGVAFICIP 89
Qy 71 LYIPHTLP-EWDGKEICVFWLTTDYLLCTASVNIYVILSYDRILSNAVSRTQHTGV 129
Db 90 LYVYVVLGRTWTFGRGCKMLVVDYLLCTSSAFNIVILSYDRILSVRAVSRAQOQNT 149
Qy 130 LKITYLWAVVAVLAFVNGPMILVSESK-----DEGSECEPGFSEWYILATISFL 181
Db 150 RRAVRKMLVWVLAFLVGPAIL---SWEYLSGSSSIPEG-HCYAEFFYNYFLTASTL 205
Qy 182 EFVLPVLIVAFNNNTY-----NSLMKRD 205
Db 206 EFFLPFLSVTFNLSIYINIORRRLRDGAREAGPEPPDAQSPPPPGCWCWKXG 265
Qy 206 HLSRCQSH-----PGLTAVSSNICGHSFRGLSSRSLSASTEVPAHSERQ 253
Db 266 HGEAMPRLHRYGVGEAAGAEGETALGCGGGGSAASPTSSSGSSSRTGTERPRSLKRSK 325
Qy 254 RRKSLMFSSRTKNSNTIASKMGFSQSDVALHOREHVELLRARLAKSLATLLGVFA 313
Db 326 PSASSASLEKMKWVSQ-----SFTQ-----RFLSRKRYAKSLAVISLIG 368
Qy 314 VCAWAPYSFTYLSFYSSTAGKSWYRIAPLQWNSFVNPL 373
Db 369 LCWAPYTLTILMIRAAACHGVCP-DYVYRTSFWLLMANSVAVPVLYPLCHSFRRAFTLL 427

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Qy 374 C---IKKOP 379
Db 428 CPQKTIQP 436

RESULT 5
US-09-165-543-5
; Sequence 5, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Gluckeman
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHYE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,543
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,780
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: NMI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-165-543-5

Query Match 36.0%; Score 729; DB 2; Length 445;
Best Local Similarity 39.1%; Pred. No. 2e-52;
Matches 166; Conservative 54; Mismatches 131; Indels 74; Gaps 10;

Qy 11 SLSTRVTTLAFMSIVAFAMIGNALVILAFVVDKMLRRSSYFFLNLAISDFVGVISIP 70
Db 30 SAATTAVALAAMALLIVATVIGNALVILAFVADSLSRTQNNFFLNLAISDFVGVAFICIP 89
Qy 71 LYIPHTLP-EWDGKEICVFWLTTDYLLCTASVNIYVILSYDRILSNAVSRTQHTGV 129
Db 90 LYVYVVLGRTWTFGRGCKMLVVDYLLCTASVNIYVILSYDRILSVRAVSRAQOQNT 149
Qy 130 LKITYLWAVVAVLAFVNGPMILVSESK-----DEGSECEPGFSEWYILATISFL 181
Db 150 RRAVRKMLVWVLAFLVGPAIL---SWEYLSGSSSIPEG-HCYAEFFYNYFLTASTL 205
Qy 182 EFVLPVLIVAFNNNTY-----NSLMKRD 205
Db 206 EFFLPFLSVTFNLSIYINIORRRLRDGAREAGPEPPDAQSPPPPGCWCWKXG 265
Qy 206 HLSRCQSH-----PGLTAVSSNICGHSFRGLSSRSLSASTEVPAHSERORRS 257
Db 266 HGEAMPRLHRYGVGEAAGAEGETALGCGGGGSAASPTSSSGSS-----SRTGTERPR 318
Qy 258 SLMFSSRTKNSNTIASKMGFSQSDVALHOREHVELLRARLAKSLATLLGVFAVCAW 317

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Db 319 SLKGRKSPASSASLEKRMKVSOSIT-----QRFSLRDKKAKSLAIIIVSIFGLCWA 372
 Qy 318 PYSLEFIVLSFYSSATGPKSVWYRIAFWLFNSFVNPLLYPLCKRFOKAFKIFC--- 374
 Db 373 PYTLIMTIRACHGRGCI-P-DWYETSFMLWMANSVNVPLVPLCHYSFRRAFTLLCPQK 431
 Qy 375 IKKQP 379
 Db 432 LKQOP 436

RESULT 6
 US-09-891-053-25
 ; Sequence 25, Application US/09891053
 ; Patent No. 6750322
 ; GENERAL INFORMATION:

APPLICANT: Itadani, Hitaru
 APPLICANT: Takimura, Tetsuo
 APPLICANT: Nakamura, Takao
 APPLICANT: Kodayashi, Masaaki
 APPLICANT: Tanaka, Ken-ichi
 APPLICANT: Hidaka, Yusuke
 APPLICANT: Ohta, Masataka
 TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
 TITLE OR INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS
 FILE REFERENCE: 06501-083001
 CURRENT APPLICATION NUMBER: US/09/891,053
 PRIOR FILING DATE: 2001-09-17
 PRIOR APPLICATION NUMBER: PCT/JP99/07280
 PRIOR FILING DATE: 1999-12-24
 PRIOR APPLICATION NUMBER: PCT/JP98/05967
 PRIOR FILING DATE: 1998-12-25
 PRIOR APPLICATION NUMBER: JP 11/145661
 PRIOR FILING DATE: 1999-05-25
 NUMBER OF SEQ ID NOS: 26
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 25
 LENGTH: 445
 TYPE: PRT
 ORGANISM: Rattus norvegicus
 US-09-891-053-25

Query Match 36.0%; Score 729; DB 2; Length 445;

Best Local Similarity 39.1%; Pred. No. 2e-52;
 Matches 166; Conservative 54; Mismatches 131; Indels 74; Gaps 10;

Qy 11 SLSTRVTLAFMSIVAFAMIGNALVILAFVVDKNLRRHSYFFLNLAISDFEFGVISIP 70
 Db 30 SAANTAVLALMALIIVATVIGNALVILAFVADSSLRTONNFILNLISDFLVGACFIP 89
 Qy 71 LYIPHTLP-EMDFGKEICVFMLTTDYLLCTASVYNIIVLISYDRYLSVSNVSYRTQHTGV 129
 Db 90 LYVPVYLGRWTFGRGCKLMLVVDYLLCASVFNIVLISYDRFLSVTRAVSYRAOQDGT 149
 Qy 130 LKTYTLMAVAVVLAFLVNGFMILVSESK-----DEGSECEGPFSEWYLAITSFL 181
 Db 150 RRAVRKXALVWVLAFLVGPAIL---SWEYLSGGSSIPDG-HCYAEFFYNNYFLITASTL 205
 Qy 182 EFVLPVILVAFNNMIY-----SLMKRD 205
 Db 206 EFPFLSVTFNLSIYANIQRTRLRDGREGAPPPDAQSPPPAPSCMCWPKG 265
 Qy 206 HLSRCQSH-----PGLTAVSSNICGHSFRGLSSRRSLASTEVASFHSERQRRKS 257
 Db 266 HGEAMPLHRYGVGEAGPVEBAGEALGGSGGGAASPSSSGSS-----SRGTERPR 318
 Qy 258 SLMFSSRTKMSNTIAKMGSPFOSDSVALHOREHVELLBARLAKSLAIIIVGAVCWA 317
 Db 319 SLKGRKSPASSASLEKRMKVSOSIT-----QRFSLRDKKAKSLAIIIVSIFGLCWA 372
 Qy 318 PYSLEFIVLSFYSSATGPKSVWYRIAFWLFNSFVNPLLYPLCKRFOKAFKIFC--- 374
 Db 373 PYTLIMTIRACHGRGCI-P-DWYETSFMLWMANSVNVPLVPLCHYSFRRAFTLLCPQK 431

Qy 375 IKKQP 379
 Db 432 LKQOP 436

RESULT 7
 US-10-453-106-3
 ; Sequence 3, Application US/10453106
 ; Patent No. 6906060
 ; GENERAL INFORMATION:

APPLICANT: Peschke, Bernd
 APPLICANT: Hohlweg, Rolf
 TITLE OF INVENTION: SUBSTITUTED HEXAHYDROPYRROLO(1,2-A)PYRAZINES,
 TITLE OR INVENTION: OCTAHYDROPYRIDO(1,2-A)PYRAZINES AND
 FILE REFERENCE: 6483,200-US
 CURRENT APPLICATION NUMBER: US/10/453,106
 PRIOR FILING DATE: 2003-06-03
 PRIOR APPLICATION NUMBER: US 60/387,047
 PRIOR FILING DATE: 2002-06-07
 PRIOR APPLICATION NUMBER: Danish Application no. PA 2002 00863
 PRIOR FILING DATE: 2002-06-06
 NUMBER OF SEQ ID NOS: 3
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 3
 LENGTH: 445
 TYPE: PRT
 ORGANISM: Rat
 US-10-453-106-3

Query Match 36.0%; Score 729; DB 2; Length 445;

Best Local Similarity 39.1%; Pred. No. 2e-52;
 Matches 166; Conservative 54; Mismatches 131; Indels 74; Gaps 10;

Qy 11 SLSTRVTLAFMSIVAFAMIGNALVILAFVVDKNLRRHSYFFLNLAISDFEFGVISIP 70
 Db 30 SAANTAVLALMALIIVATVIGNALVILAFVADSSLRTONNFILNLISDFLVGACFIP 89
 Qy 71 LYIPHTLP-EMDFGKEICVFMLTTDYLLCTASVYNIIVLISYDRYLSVSNVSYRTQHTGV 129
 Db 90 LYVPVYLGRWTFGRGCKLMLVVDYLLCASVFNIVLISYDRFLSVTRAVSYRAOQDGT 149
 Qy 130 LKTYTLMAVAVVLAFLVNGFMILVSESK-----DEGSECEGPFSEWYLAITSFL 181
 Db 150 RRAVRKXALVWVLAFLVGPAIL---SWEYLSGGSSIPDG-HCYAEFFYNNYFLITASTL 205
 Qy 182 EFVLPVILVAFNNMIY-----SLMKRD 205
 Db 206 EFPFLSVTFNLSIYANIQRTRLRDGREGAPPPDAQSPPPAPSCMCWPKG 265
 Qy 206 HLSRCQSH-----PGLTAVSSNICGHSFRGLSSRRSLASTEVASFHSERQRRKS 257
 Db 266 HGEAMPLHRYGVGEAGPVEBAGEALGGSGGGAASPSSSGSS-----SRGTERPR 318
 Qy 258 SLMFSSRTKMSNTIAKMGSPFOSDSVALHOREHVELLBARLAKSLAIIIVGAVCWA 317
 Db 319 SLKGRKSPASSASLEKRMKVSOSIT-----QRFSLRDKKAKSLAIIIVSIFGLCWA 372
 Qy 318 PYSLEFIVLSFYSSATGPKSVWYRIAFWLFNSFVNPLLYPLCKRFOKAFKIFC--- 374
 Db 373 PYTLIMTIRACHGRGCI-P-DWYETSFMLWMANSVNVPLVPLCHYSFRRAFTLLCPQK 431
 Qy 375 IKKQP 379
 Db 432 LKQOP 436

RESULT 8
 US-08-985-090-2
 ; Sequence 2, Application US/08985090
 ; Patent No. 5885893
 ; GENERAL INFORMATION:

APPLICANT: Andrew D.J. Goodearl
 TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
 NUMBER OF SEQUENCES: 28
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD, LLP
 STREET: 28 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/985,090
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Jean M. Silveri
 REGISTRATION NUMBER: 39,030
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400
 TELEFAX: (617)742-4214
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 445 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-985-090-2

Query Match 35.8%; Score 724; DB 1; Length 445;
 Best Local Similarity 38.6%; Pred. No. 5.2e-52;
 Matches 164; Conservative 56; Mismatches 131; Indels 74; Gaps 10;

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QY 11 SLSTRVTLAFMNSVAFAMLGNALVTLAFVVDKNLRRSSYFFLNLAISDFEYGVISIP 70
DB 30 SAAMTAVLALMALIIVATVGNALVAFVADSSLRTONNFFLNLAISDFLVGAFICP 89
QY 71 LYIPHTLF-EMDEGKEICVFWLTTDYLLCTASVYNTVILSYDRYLSVSNVSYRTQHTGV 129
DB 90 LYVPYVLTGRNTPGRGLCKMLVVDYLLCTSSAFNIVILSYDRFLSVTRAVSYRAQGGDT 149
QY 130 LKIVTLVAVVTLAFVNGPMILVSESWK-----DESECEBPGFSEMYIIAITSFL 181
DB 150 RRAVRKMLVWVLAFLVLYGPAIL---SWEYLSGGSSIPFG-HCYAEFFNMYFLITASTL 205
QY 182 EFVYIPVLVAVFNNNTY-----WSLWKRD 205
DB 206 EFTFPFLSVTFEINSLIYNTIQRTRLRDGAREAGPEPPPEAOPSPPPPGCGKCGK 265
QY 206 HLSRCOSH-----PGLTAVSSNICGHSFRGLSSRRSLASTEVPAFSHERQRKS 257
DB 266 HGEAMPFHRVGVGEAAVGAEGEATLGGGGGGSVASPTSSGSS-----SRGTERPR 318
QY 258 SLMFSSRTKNSNTIASKGSPFQSDSVLAHQREHVELLRARLAKSLAILLGVFAVCWA 317
DB 319 SLKRGSKPSASSASLEKRMKVVSQSF-----QRFRLSDRKAASLAVIVSIFGLCWA 372
QY 318 PYSLFTVLVSFYSSATGPKSVWYRIAFWLOWFNSFVNPLLYPLCHKRFQKAFLEIFC--- 374
DB 373 PYTELMIIRAAAGHGVCP-DYWTETSEWLMANSAVNPVLYPLCHHSFRRAFTLLCPQK 431
QY 375 IKKOP 379
DB 432 LKIQP 436

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RESULT 9

US-09-165-543-2

Sequence 2, Application US/09165543

Patent No. 6093545

GENERAL INFORMATION:

APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann

TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD, LLP

STREET: 28 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/165,543

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/042,780

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Elizabeth A. Hanley

REGISTRATION NUMBER: 33,505

REFERENCE/DOCKET NUMBER: NMT-032CP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 445 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-165-543-2

Query Match 35.8%; Score 724; DB 2; Length 445;

Best Local Similarity 38.6%; Pred. No. 5.2e-52;

Matches 164; Conservative 56; Mismatches 131; Indels 74; Gaps 10;

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QY 11 SLSTRVTLAFMNSVAFAMLGNALVTLAFVVDKNLRRSSYFFLNLAISDFEYGVISIP 70
DB 30 SAAMTAVLALMALIIVATVGNALVAFVADSSLRTONNFFLNLAISDFLVGAFICP 89
QY 71 LYIPHTLF-EMDEGKEICVFWLTTDYLLCTASVYNTVILSYDRYLSVSNVSYRTQHTGV 129
DB 90 LYVPYVLTGRNTPGRGLCKMLVVDYLLCTSSAFNIVILSYDRFLSVTRAVSYRAQGGDT 149
QY 130 LKIVTLVAVVTLAFVNGPMILVSESWK-----DESECEBPGFSEMYIIAITSFL 181
DB 150 RRAVRKMLVWVLAFLVLYGPAIL---SWEYLSGGSSIPFG-HCYAEFFNMYFLITASTL 205
QY 182 EFVYIPVLVAVFNNNTY-----WSLWKRD 205
DB 206 EFTFPFLSVTFEINSLIYNTIQRTRLRDGAREAGPEPPPEAOPSPPPPGCGKCGK 265
QY 206 HLSRCOSH-----PGLTAVSSNICGHSFRGLSSRRSLASTEVPAFSHERQRKS 257
DB 266 HGEAMPFHRVGVGEAAVGAEGEATLGGGGGGSVASPTSSGSS-----SRGTERPR 318
QY 258 SLMFSSRTKNSNTIASKGSPFQSDSVLAHQREHVELLRARLAKSLAILLGVFAVCWA 317
DB 319 SLKRGSKPSASSASLEKRMKVVSQSF-----QRFRLSDRKAASLAVIVSIFGLCWA 372
QY 318 PYSLFTVLVSFYSSATGPKSVWYRIAFWLOWFNSFVNPLLYPLCHKRFQKAFLEIFC--- 374
DB 373 PYTELMIIRAAAGHGVCP-DYWTETSEWLMANSAVNPVLYPLCHHSFRRAFTLLCPQK 431

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QY 375 IKKOP 379
 DB 432 LKTOP 436

RESULT 10

US-09-167-354-7

Sequence 7, Application US/09167354A

Patent No. 6136559

GENERAL INFORMATION:

APPLICANT: Erlander, Mark

APPLICANT: Pyati, Jayashree

APPLICANT: Huvar, Arne

TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3

FILE REFERENCE: JMW

CURRENT APPLICATION NUMBER: US/09/167,354A

PRIORITY FILING DATE: 1998-10-07

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 7

LENGTH: 445

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: PEPTIDE

US-09-167-354-7

Query Match 35.8%; Score 724; DB 2; Length 445;

Best Local Similarity 38.6%; Pred. No. 5.2e-52; Indels 74; Gaps 10;

Matches 164; Conservative 56; Mismatches 131;

QY 11 SLSTRVTIAFMSLVAFAIMGNALVIAFVVDKRLHRSYFELNLATSDPFVGVISIP 70
 DB 30 SAAMTAVIALMALVIAVTVLGNALVIAFVADSSLRQNNFELNLATSDPLVGAFICP 89
 QY 71 LYIPHTLF-EWDGKEICVFWLTTDYLLCTASVYNIIVLISYDRYLSVSNVSYRTHGTG 129
 DB 90 LYPVYVLTGRWTFGRGLCKMLVVDYLLCTSSAFNIIVLISYDRFLSVTRAVSYRAOQGD 149
 QY 130 LKVTLMVAVMTALFVNGPMILVSESWK-----DGSCEBPFPFSEWYLLATISFL 181
 DB 150 RRAVRKMLVAVMTALFVNGPMILVSESWK-----DGSCEBPFPFSEWYLLATISFL 205
 QY 182 EFVTPVILVAFVFNMIY-----WLSWKRD 205
 DB 206 EFTFPFLSTYFPLSTYIYNIQRTRLRLDGRARAEAPPEPPAQPSPPPPGCMGCKQKG 265
 QY 206 HLSRCQSH-----PGLTAVSSNICGHSFRGLSRRLSASTEVPAFHSERQRRKS 257
 DB 266 HGEAMPFHRVGVGEAAGVAGATLGGGGGGGVSAPSSSGSS-----SRGTERPR 318
 QY 258 SLMFSSRTKMSNTTASKSGSFQSDSVLAHQREHVELLRARLAKSLAILGVFAVCMA 317
 DB 319 SLKRGSKPSSASSLSEKMKMVSQSF-----QRFRLSRDRKVAKSLAVISIFGLCMA 372
 QY 318 PYSLFTIVLSFYSSATGPKSVWYRIAFWLMQFNSFVNPPLYPLCHKRFQKAFKIFC--- 374
 DB 373 PYTLMTIIRAACHGCHVP-DYWTETSFMLMANSVAVNPVLYPLCHSFRRAFTLCLCPQK 431
 QY 375 IKKOP 379
 DB 432 LKTOP 436

RESULT 11

US-09-642-855-7

Sequence 7, Application US/09642855

Patent No. 6413743

GENERAL INFORMATION:

APPLICANT: Erlander, Mark

APPLICANT: Pyati, Jayashree

APPLICANT: Huvar, Arne

TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3

FILE REFERENCE: JMW

CURRENT APPLICATION NUMBER: US/09/167,354A

PRIORITY FILING DATE: 1998-10-07

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 7

LENGTH: 445

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: PEPTIDE

US-09-167-354-7

Query Match 35.8%; Score 724; DB 2; Length 445;

Best Local Similarity 38.6%; Pred. No. 5.2e-52; Indels 74; Gaps 10;

Matches 164; Conservative 56; Mismatches 131;

QY 11 SLSTRVTIAFMSLVAFAIMGNALVIAFVVDKRLHRSYFELNLATSDPFVGVISIP 70

DB 30 SAAMTAVIALMALVIAVTVLGNALVIAFVADSSLRQNNFELNLATSDPLVGAFICP 89

QY 71 LYIPHTLF-EWDGKEICVFWLTTDYLLCTASVYNIIVLISYDRYLSVSNVSYRTHGTG 129

DB 90 LYPVYVLTGRWTFGRGLCKMLVVDYLLCTSSAFNIIVLISYDRFLSVTRAVSYRAOQGD 149

QY 130 LKVTLMVAVMTALFVNGPMILVSESWK-----DGSCEBPFPFSEWYLLATISFL 181

DB 150 RRAVRKMLVAVMTALFVNGPMILVSESWK-----DGSCEBPFPFSEWYLLATISFL 205

QY 182 EFVTPVILVAFVFNMIY-----WLSWKRD 205

DB 206 EFTFPFLSTYFPLSTYIYNIQRTRLRLDGRARAEAPPEPPAQPSPPPPGCMGCKQKG 265

QY 206 HLSRCQSH-----PGLTAVSSNICGHSFRGLSRRLSASTEVPAFHSERQRRKS 257

DB 266 HGEAMPFHRVGVGEAAGVAGATLGGGGGGGVSAPSSSGSS-----SRGTERPR 318

QY 258 SLMFSSRTKMSNTTASKSGSFQSDSVLAHQREHVELLRARLAKSLAILGVFAVCMA 317

DB 319 SLKRGSKPSSASSLSEKMKMVSQSF-----QRFRLSRDRKVAKSLAVISIFGLCMA 372

QY 318 PYSLFTIVLSFYSSATGPKSVWYRIAFWLMQFNSFVNPPLYPLCHKRFQKAFKIFC--- 374

DB 373 PYTLMTIIRAACHGCHVP-DYWTETSFMLMANSVAVNPVLYPLCHSFRRAFTLCLCPQK 431

QY 375 IKKOP 379

DB 432 LKTOP 436

RESULT 12

US-09-642-855-7

Sequence 7, Application US/09642514

Patent No. 6437100

GENERAL INFORMATION:

APPLICANT: Erlander, Mark

APPLICANT: Pyati, Jayashree

APPLICANT: Huvar, Arne

TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3

FILE REFERENCE: JMW

CURRENT APPLICATION NUMBER: US/09/642,514

PRIORITY FILING DATE: 2000-08-21

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 7

LENGTH: 445

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: PEPTIDE

US-09-642-855-7

Query Match 35.8%; Score 724; DB 2; Length 445;

Best Local Similarity 38.6%; Pred. No. 5.2e-52; Indels 74; Gaps 10;

Matches 164; Conservative 56; Mismatches 131;

QY 11 SLSTRVTIAFMSLVAFAIMGNALVIAFVVDKRLHRSYFELNLATSDPFVGVISIP 70

DB 30 SAAMTAVIALMALVIAVTVLGNALVIAFVADSSLRQNNFELNLATSDPLVGAFICP 89

QY 71 LYIPHTLF-EWDGKEICVFWLTTDYLLCTASVYNIIVLISYDRYLSVSNVSYRTHGTG 129

DB 90 LYPVYVLTGRWTFGRGLCKMLVVDYLLCTSSAFNIIVLISYDRFLSVTRAVSYRAOQGD 149

QY 130 LKVTLMVAVMTALFVNGPMILVSESWK-----DGSCEBPFPFSEWYLLATISFL 181

DB 150 RRAVRKMLVAVMTALFVNGPMILVSESWK-----DGSCEBPFPFSEWYLLATISFL 205

QY 182 EFVTPVILVAFVFNMIY-----WLSWKRD 205

DB 206 EFTFPFLSTYFPLSTYIYNIQRTRLRLDGRARAEAPPEPPAQPSPPPPGCMGCKQKG 265

QY 206 HLSRCQSH-----PGLTAVSSNICGHSFRGLSRRLSASTEVPAFHSERQRRKS 257

DB 266 HGEAMPFHRVGVGEAAGVAGATLGGGGGGGVSAPSSSGSS-----SRGTERPR 318

QY 258 SLMFSSRTKMSNTTASKSGSFQSDSVLAHQREHVELLRARLAKSLAILGVFAVCMA 317

DB 319 SLKRGSKPSSASSLSEKMKMVSQSF-----QRFRLSRDRKVAKSLAVISIFGLCMA 372

QY 318 PYSLFTIVLSFYSSATGPKSVWYRIAFWLMQFNSFVNPPLYPLCHKRFQKAFKIFC--- 374

DB 373 PYTLMTIIRAACHGCHVP-DYWTETSFMLMANSVAVNPVLYPLCHSFRRAFTLCLCPQK 431

QY 375 IKKOP 379

DB 432 LKTOP 436

RESULT 12

US-09-642-855-7

Sequence 7, Application US/09642514

Patent No. 6437100

GENERAL INFORMATION:

APPLICANT: Erlander, Mark

APPLICANT: Pyati, Jayashree

APPLICANT: Huvar, Arne

TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3

FILE REFERENCE: JMW

CURRENT APPLICATION NUMBER: US/09/642,514

PRIORITY FILING DATE: 2000-08-21

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 7

LENGTH: 445

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: PEPTIDE

US-09-642-855-7

Query Match 35.8%; Score 724; DB 2; Length 445;

Best Local Similarity 38.6%; Pred. No. 5.2e-52; Indels 74; Gaps 10;

Matches 164; Conservative 56; Mismatches 131;

QY 11 SLSTRVTIAFMSLVAFAIMGNALVIAFVVDKRLHRSYFELNLATSDPFVGVISIP 70

DB 30 SAAMTAVIALMALVIAVTVLGNALVIAFVADSSLRQNNFELNLATSDPLVGAFICP 89

QY 71 LYIPHTLF-EWDGKEICVFWLTTDYLLCTASVYNIIVLISYDRYLSVSNVSYRTHGTG 129

DB 90 LYPVYVLTGRWTFGRGLCKMLVVDYLLCTSSAFNIIVLISYDRFLSVTRAVSYRAOQGD 149

QY 130 LKVTLMVAVMTALFVNGPMILVSESWK-----DGSCEBPFPFSEWYLLATISFL 181

DB 150 RRAVRKMLVAVMTALFVNGPMILVSESWK-----DGSCEBPFPFSEWYLLATISFL 205

QY 182 EFVTPVILVAFVFNMIY-----WLSWKRD 205

DB 206 EFTFPFLSTYFPLSTYIYNIQRTRLRLDGRARAEAPPEPPAQPSPPPPGCMGCKQKG 265

QY 206 HLSRCQSH-----PGLTAVSSNICGHSFRGLSRRLSASTEVPAFHSERQRRKS 257

DB 266 HGEAMPFHRVGVGEAAGVAGATLGGGGGGGVSAPSSSGSS-----SRGTERPR 318

QY 258 SLMFSSRTKMSNTTASKSGSFQSDSVLAHQREHVELLRARLAKSLAILGVFAVCMA 317

DB 319 SLKRGSKPSSASSLSEKMKMVSQSF-----QRFRLSRDRKVAKSLAVISIFGLCMA 372

QY 318 PYSLFTIVLSFYSSATGPKSVWYRIAFWLMQFNSFVNPPLYPLCHKRFQKAFKIFC--- 374

DB 373 PYTLMTIIRAACHGCHVP-DYWTETSFMLMANSVAVNPVLYPLCHSFRRAFTLCLCPQK 431

QY 375 IKKOP 379

DB 432 LKTOP 436


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1  NUMBER OF SEQ ID NOS: 8
2  SOFTWARE: PatentIn Ver. 2.0
3  SEQ ID NO 7
4  LENGTH: 445
5  TYPE: PRT
6  ORGANISM: Artificial Sequence
7  FEATURE:
8  OTHER INFORMATION: Description of Artificial Sequence: PEPTIDE
9  OS-09-642-514-7

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Query Match	35.8%	Score 724;	DB 2;	Length 445;
Best Local Similarity	38.6%;	Pred. No. 5.2e-52;		
*Matches 164;	Conservative 56;	Mismatches 131;	Indels 74;	Gaps 10;

Qy	11	SLSTRVTLAFENSLVAFNMGALVTLFVVDKMLRHRSYFFNLNLAISDFPVGVISIP	70
Db	30	SAAMTAVIALMALMLIVATVIGNALVMLAFVADSSLRQNPNFFLNLAISDFLVGARCIP	89
Qy	71	LYIPHLF--EMDGKEICVFMULTTDTLLCTASVNIVLISIDRYLSUSNAVSYTQHTGV	129
Db	90	LYPYVYLGTMRGTGRGLCKTLMVVDLLCTSSAFNIVLISYRFLSSVLRAYSYPAAQGDTR	149
Qy	130	LKIVTLVAWVWTLAFVNGPMILVSESNK-----DEGSECEGPFSEWYILAIISFL	181
Db	150	RRAVRKMLVWVWTLAFVNGPAIL--SWEYLSGGSSIPBG--HCTAEFFYNNYFLITSTL	205
Qy	182	EFVYPIVLAAYFNMMNY-----MSLWRKD	205
Db	206	EFTTFPLSTVTFNLSIYLNIGQRTRLRLDGAEEAGPEPPPEAQQSPPPPGCGMGCKDG	265
Qy	206	HLSCRQSH-----PGLTAVSNINCGHSFPGRLSSRRSLASTGEVPAHFSERQRRKS	257
Db	266	HGEAMPLHRVYGEAAVGAAGBATVGGGGGGGSAVASTSSSGS-----SRGTERPR	318
Qy	258	SLMFSSRTKQNSVNTIASKMGSPQSDSVMLHGRHEVELLRARLAKSLALILGVPAWCMA	317
Db	319	SLRGSGKPSASSASLEKRRKQMSQST-----QAFRLSRDRKAKSLAVVSIIFGLCMA	372
Qy	318	PVSLFTIVLSFYSSATGPKSVWYRIAFWLQWFNSFVNPLLYPLCHKRFQKAFIKFC--	374
Db	373	PYTLMIIRACGHGCVPR--DYWYETSFMLLMANSAVNPLVPLCHSFPRAFTYLLCPQK	431
Qy	375	IKKQIP	379
Db	432	LKIQP	436

```

RESULT 13
US-09-642-852-7
/ Sequence 7, Application US/09642852
/ Patent No. 6855560
/ GENERAL INFORMATION:
/ APPLICANT: Lovenberg, Timothy
/ APPLICANT: Erlander, Mark
/ APPLICANT: Pyatt, Jayashree
/ APPLICANT: Havat, Arne
/ TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
/ TITLE OF INVENTION: SUBTYPE
/ FILE REFERENCE: JMW
/ CURRENT APPLICATION NUMBER: US/09/642,852
/ CURRENT FILING DATE: 2000-08-21
/ PRIOR APPLICATION NUMBER: 09/167,354
/ PRIOR FILING DATE: 1998-10-07
/ NUMBER OF SEQ. ID NOS: 8
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 7
/ LENGTH: 445
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:PEPTIDE
US-09-642-852-7

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Query Match	35.8%;	Score 724;	DB 2;	Length 445;
Best Local Similarity	38.6%;	Pred. No. 5.2e-52;		
Matches 164;	Conservative 56;	Mismatches 131;	Indels 74;	Gaps 10;

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QY      11 SLSTVTTLAFMFSLVAFPAIMGNALVILAFVVDKMLRRHSYFFNLATISDFVGVISIP 70
Db      30 SAAMTAVIALAAMALLIVATVIGNALVMLAFVADSSLRQNNFFLNTALISDFLVGAFCIP 89
QY      71 LYIPHTLE-EWDGKEICEVFWLTTDYLLCTASVNIIVLISYDRYISVSNASVYRTQHTGV 129
Db      90 LVPFVTLGRMTFGGRGLCKMLVMDYLLCTSSAFNIVLISYDRFSLVTAASVYRAQQCDT 149
QY      130 LKIVTLVAAVWVLAFLVNGSPMLVSESWK-----DEGSECEBPFPSEWYTLATSL 181
Db      150 RRAVRKMLLVWVLAFLVGPAIL---SNEYLSGSSSIEBG-HCYAEFFNWIPLITASTL 205
QY      182 EFVLPVILVAVFNNMNY-----WSLWKED 205
Db      206 EFPFPELSVTFEPFNLSIYNIQRTRLRLDGAEREAAGPEPPPEAPQSPPPPCGCMGCMQK 265
QY      206 HLSRCQSH-----PGLTAVSSNICGHSFRGLSSRSLSASPEVPASHSEQRKRS 257
Db      266 HGEAMPLRHYVGVEAAGAEAGELTLGGGGGGGGSVASPTSSGGS-----SRGTERPR 318
QY      258 SLMFSSRTKQNSNTLTASRCGSPFOSDSVALHOREHEVELLRARLRLKSLATILGVPAVCWA 317
Db      319 SLKRGSKRSASASLSERKMKRVQSFT-----QKFRLSRDKVAKSLAVIYSIFELCWA 372
QY      318 PYSLEFTLVSYSSATGPKSVWYRIAFMLQWFNSEVFNPLIYPLCHKRQKAFKIFC--- 374
Db      373 PYTLIMTIRACCHGCHVP-DYWEYTESFWILTMANSVNVNLYPLCHHSFRAPFTKLLCPQK 431
QY      375 IKKOP 379
Db      432 LKIQP 436

```

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RESULT 14
US-10-453-106-1
; Sequence 1, Application US/10453106
; Patent No. 6906060
; GENERAL INFORMATION:
; APPLICANT: Peschke, Bernd
; APPLICANT: Hohlweg, Rolf
; TITLE OF INVENTION: SUBSTITUTED HEXAHYDROPYRROLO[1,2-a]PYRAZINES,
; TITLE OF INVENTION: OCTAHYDROPYRIDO[1,2-a]PYRAZINES AND
; TITLE OF INVENTION: DECAHYDROPYRAZINO[1,2-a]AZEPINES
; FILE REFERENCE: 6483,200-US
; CURRENT APPLICATION NUMBER: US/10/453,106
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: US 60/367,047
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: Danish Application no. PA 2002 00863
; PRIOR FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-10-453-106-1

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Query Match	35.8%;	Score 724;	DB 2;	Length 445;
Best Local Similarity	38.6%;	Pred. No. 5.2e-52;		
Matches 164;	Conservative 56;	Mismatches 131;	Indels 74;	Gaps 10;

[illegible]

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QY      130 LKIITLWVAWVLAFLVNGPMLIVSESXK-----DGGSECEPPFEEWYLIATSTPL 181
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      150 RRAVRKMLLVWVLAFLVLPAIL---SWEYLSGSSIPPEG-HCYAEFFWVIFLIATSTL 205
QY      182 EFVLPVILVAYFNNNY-----WSLWKKD 205
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      206 EFFFPLPVLTFEFNLSITLYINQRTRLRLDGAEGAPEDPEPEAOPPPPPCGCMQCKG 265
QY      206 HLSRCQSH-----PGLTAVSNSI CGHSFPGRLSSRRSLASCTEVPASPHSERORRKS 257
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      266 HGEAMPLHRYGVGAAYGAEAGEATLGCGGCGGSVASPTSSSGSS-----SRGTERRR 318
QY      258 SLMSSSRRKNXNSNTLASKKGSFSGSDSVALLHOREHYELLRARRLASLAILCGFAVCA 317
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      319 SLKSGSKSPASASLEKRMKXVOSQFT-----QRFRLSRDRKXAKSLAVIYSIFELCWA 372
QY      318 PYSLFTIYLSFYSASATGPKSVWYRTLAFLWQFNSFNPPLLPLCHRRFOKAFIKTIC--- 374
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      373 PYTLIMITIRAACHGHCVP-DYWEYTSFWLLMANSANVPVLYPLCHHSFRFAFTKCLCPQK 431
QY      375 IKKOP 379
      : : : : :
Db      432 LKIQP 436

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RESULT 15
US-09-949-016-10930
; Sequence 10930, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10930
; LENGTH: 449
; TYPE: PR1
; ORGANISM: Human
; US-09-949-016-10930

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Query Match	35.8%;	Score 724;	DB 2;	Length 449;
Best Local Similarity	38.6%;	Pred. No. 5.3e-52;		
Matches 164;	Conservative 56;	Mismatches 131;	Indels 74;	Gaps 10;

[illegible]

Db 270 HGEAMPELRHYGVGBAAVGAABGEANTLGGCGGGGGSVAAPTSSGGSS-----SRGTERPR 332
 QY 258 SLMFSSRTKMANNTTASTKMGSPSGSDSYALHQRHVELLARRLAKSLALLLGVPANCA 317
 Db 323 SLRGGSKPEASASLEKEMKRVSSOSFT-----ORFLSDRKVAKSLAIVISIFGLCWA 376
 QY 318 PYSLEPIYVSPFSATGPKSVWYRIAPFLQWFNSFVNPPLLYPLCHKRFQAKFLKIFC--- 374
 Db 377 PFTLMTIIPAAAGHCHP-DYWTSTSEFLMANSANVPVLPICHSFRDAFTKLDCPQK 435
 QY 375 IKKQK 379
 Db 436 LKIQP 440

Search completed: March 28, 2006, 14:00:09
Job time : 49 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 28, 2006, 13:59:30 ; Search time 166 Seconds
(without alignments)
981.647 Million cell updates/sec.

Title: US-10-616-088-2

Perfect score: 1 MPDINSTINSLSTRVTIAF.....KIFCIKQPLPSCHSRSSVS 390

Sequence: 1 MPDINSTINSLSTRVTIAF.....KIFCIKQPLPSCHSRSSVS 390

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications NA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBSCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBSCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBSCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBSCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2024	100.0	390	US-09-812-216-2	Sequence 2, Appl1
2	2024	100.0	390	US-09-910-411-2	Sequence 2, Appl1
3	2024	100.0	390	US-09-875-076-14	Sequence 14, Appl1
4	2024	100.0	390	US-09-876-252-14	Sequence 14, Appl1
5	2024	100.0	390	US-09-852-165-2	Sequence 2, Appl1
6	2024	100.0	390	US-09-891-138A-6	Sequence 6, Appl1
7	2024	100.0	390	US-10-052-193-2	Sequence 2, Appl1
8	2024	100.0	390	US-10-225-567A-629	Sequence 629, Appl1
9	2024	100.0	390	US-10-272-983-14	Sequence 14, Appl1
10	2024	100.0	390	US-10-354-769-2	Sequence 2, Appl1
11	2024	100.0	390	US-10-393-807-14	Sequence 14, Appl1
12	2024	100.0	390	US-10-417-820A-14	Sequence 14, Appl1
13	2024	100.0	390	US-10-349-253A-2	Sequence 2, Appl1
14	2024	100.0	390	US-10-696-673-2	Sequence 2, Appl1
15	2024	100.0	390	US-10-723-955-14	Sequence 14, Appl1
16	2024	100.0	390	US-10-782-596-14	Sequence 14, Appl1
17	2024	100.0	390	US-10-777-619-2	Sequence 2, Appl1
18	2024	100.0	390	US-10-626-445-2	Sequence 2, Appl1
19	2024	100.0	390	US-10-684-206-20	Sequence 20, Appl1
20	2024	100.0	390	US-10-616-088-2	Sequence 2, Appl1
21	2024	100.0	390	US-10-626-126-2	Sequence 2, Appl1
22	2024	100.0	390	US-10-626-398-2	Sequence 2, Appl1
23	2024	100.0	390	US-10-756-149-4702	Sequence 4702, Appl1
24	2024	100.0	390	US-10-723-955-14	Sequence 14, Appl1
25	2024	100.0	390	US-10-488-421-8	Sequence 8, Appl1
26	2008	99.2	390	US-10-290-078-27	Sequence 27, Appl1
27	2008	99.2	390	US-10-488-421-6	Sequence 6, Appl1

28	1815.5	89.7	357	5	US-10-488-421-4	Sequence 4, Appl1
29	1671	82.6	336	5	US-10-488-421-2	Sequence 2, Appl1
30	1403.5	69.3	391	5	US-10-626-445-9	Sequence 9, Appl1
31	1403.5	69.3	391	5	US-10-626-126-9	Sequence 9, Appl1
32	1403.5	69.3	391	5	US-10-626-398-9	Sequence 9, Appl1
33	1370.5	67.7	391	5	US-10-626-445-8	Sequence 8, Appl1
34	1370.5	67.7	391	5	US-10-626-126-8	Sequence 8, Appl1
35	1370.5	67.7	391	5	US-10-626-398-8	Sequence 8, Appl1
36	1308.5	64.6	389	5	US-10-626-445-10	Sequence 10, Appl1
37	1308.5	64.6	389	5	US-10-626-126-10	Sequence 10, Appl1
38	1308.5	64.6	389	5	US-10-626-398-10	Sequence 10, Appl1
39	772	38.1	441	4	US-10-398-036-3	Sequence 3, Appl1
40	730	36.1	445	5	US-10-495-679A-8	Sequence 8, Appl1
41	730	36.1	445	4	US-10-453-106-2	Sequence 2, Appl1
42	730	36.1	445	5	US-10-735-963-2	Sequence 2, Appl1
43	729	36.0	445	3	US-09-891-053-25	Sequence 25, Appl1
44	729	36.0	445	3	US-09-350-206-5	Sequence 5, Appl1
45	729	36.0	445	3	US-09-349-755-5	Sequence 5, Appl1

ALIGNMENTS

RESULT 1

US-09-812-216-2

Sequence 2, Application US/09812216

Publication No. US20020098539A1

GENERAL INFORMATION:

APPLICANT: Benan, Jiang Xu

APPLICANT: Hedrick, Joseph A.

APPLICANT: Laz, Thomas M.

APPLICANT: Monsma, Frederick J. Jr.

APPLICANT: Morse, Kelley L.

APPLICANT: Umada, Shelby P.

APPLICANT: Wang, Suke

TITLE OF INVENTION: Histamine receptor

FILE REFERENCE: CNO1069

CURRENT APPLICATION NUMBER: US/09/812,216

CURRENT FILING DATE: 2001-03-19

PRIOR APPLICATION NUMBER: 09/414,010

PRIOR FILING DATE: 1999-10-07

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 390

TYPE: PRT

ORGANISM: Homo sapiens

US-09-812-216-2

Query Match 100.0%; Score 2024; DB 3; Length 390;

Best Local Similarity 100.0%; Pred. No. 1,4e-173; Mismatches 0; Indels 0; Gaps 0;

Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MPDINSTINSLSTRVTIAFMSLVAFAIMLGNALVILAFVVDKNLHRSSEYFLNLAIS	60
DB	1	MPDINSTINSLSTRVTIAFMSLVAFAIMLGNALVILAFVVDKNLHRSSEYFLNLAIS	60
QY	61	DFVGVISIPLYIPHTLFEWDFGKEICVFMLTDDYLCTASVNIYVLSYDRYLSVNAV	120
DB	61	DFVGVISIPLYIPHTLFEWDFGKEICVFMLTDDYLCTASVNIYVLSYDRYLSVNAV	120
QY	121	SYTQHTGVLKTYTLMAVAVVLAFLVNGPMIIVSESKRGSCPEPFSEWYLAITSF	180
DB	121	SYTQHTGVLKTYTLMAVAVVLAFLVNGPMIIVSESKRGSCPEPFSEWYLAITSF	180
QY	181	LEFVIVILVAYENNMNIYMSLWKRDLISRCQSHPGTLAVSNICGHSFRGLSSRSLSA	240
DB	181	LEFVIVILVAYENNMNIYMSLWKRDLISRCQSHPGTLAVSNICGHSFRGLSSRSLSA	240
QY	241	STVPVASFSESRQRKSSLMFSSRTKNSNTTASKNGSFGQSVALHQREHYELFARR	300
DB	241	STVPVASFSESRQRKSSLMFSSRTKNSNTTASKNGSFGQSVALHQREHYELFARR	300

Qy	30	LASLAILLLGVFAVCAPSLFLTYLSFFSSATGPGSWYRIAFMLQNFNSFNPLLYPL	360
Dd	301	LASLAIILLGVFAVCAPSLFLTYLSFFSSATGPGSWYRIAFMLQNFNSFNPLLYPL	360
Qy	361	CHRRFOKALPILKICIKKOPLPSSHHSVSS	390
Dd	361	CHRRFOKALPILKICIKKOPLPSSHHSVSS	390

RESULT 2
US-09-910-411-2

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Sequence 2, Application US/09910411
Patent No. US20020137054A1
GENERAL INFORMATION:
APPLICANT: Bergsma, Bert
APPLICANT: Fitzgerald, Laura
APPLICANT: Li, Xiaotong
APPLICANT: Michalovich, David
APPLICANT: Zhu, Yuan
TITLE OR INVENTION: AOR35, A G-Protein Coupled Receptor
FILE REFERENCE: GP070655-201
CURRENT APPLICATION NUMBER: US/09/910,411
CURRENT FILING DATE: 2001-07-20
PRIORITY APPLICATION NUMBER: 09/693,761
PRIORITY FILING DATE: 2000-10-20
PRIORITY APPLICATION NUMBER: 09/497,790
PRIORITY FILING DATE: 2000-02-03
PRIORITY APPLICATION NUMBER: 09/431,898
PRIORITY FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 390
TYPE: PRT
ORGANISM: Homo sapien
US-09-910-411-2

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Query Match	100.0%	Score 2024	DB 3	Length 390
Best Local Similarity	100.0%	Prod. No.	1.4e-173	
Matches 390	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Qy	1	MPDNTSGINILNLSSTRVTLVLFPMNSLVAFAMLNALVILAFVVDKULRRSRSSFFNLIAIS	60
Db	1	MPDNTSGINILNLSSTRVTLVLFPMNSLVAFAMLNALVILAFVVDKULRRSRSSFFNLIAIS	60
Qy	61	DPEVGVISIPLYIPHTLFEWDFEKEICVEMLTTDYLLCTASVYINVLISYDRYLSVSNV	120
Db	61	DPEVGVISIPLYIPHTLFEWDFEKEICVEMLTTDYLLCTASVYINVLISYDRYLSVSNV	120
Qy	121	SYRTQHTGVLTIVTLMAVAVVTLAEVLNGEMILVSESKWDEGECEGPGFSEMYLIATISF	180
Db	121	SYRTQHTGVLTIVTLMAVAVVTLAEVLNGEMILVSESKWDEGECEGPGFSEMYLIATISF	180
Qy	181	LEEVIPILIVAYFNNMIYMSLWKRDLSPCOSHPGLTAVSSNICGHSFRGLSSRRSLSA	240
Db	181	LEEVIPILIVAYFNNMIYMSLWKRDLSPCOSHPGLTAVSSNICGHSFRGLSSRRSLSA	240
Qy	241	STEVPASFHSERORRKSILMFSSRTQMSNTIASKKSGSPQSDSVALLQREHVELLRARR	300
Db	241	STEVPASFHSERORRKSILMFSSRTQMSNTIASKKSGSPQSDSVALLQREHVELLRARR	300
Qy	301	LAKSLAILLGVFAVCAPYSLFTIVLSFYSSATGPKSVYRIAPLQMFNSFVNPDLVPL	360
Db	301	LAKSLAILLGVFAVCAPYSLFTIVLSFYSSATGPKSVYRIAPLQMFNSFVNPDLVPL	360
Qy	361	CHKRFQAKIFICIKKQPLPSQHSRSVS	390
Db	361	CHKRFQAKIFICIKKQPLPSQHSRSVS	390

RESULT 3
US-09-875-076-14
; Sequence 14, Application US/09875076

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Publication No.: US20030017528A1
GENERAL INFORMATION:
APPLICANT: Chen, Ruoping
APPLICANT: Dang, Huong T.
APPLICANT: Liaw, Chen W.
APPLICANT: Lin, I-Lin
TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
FILE REFERENCE: AREN0050
CURRENT APPLICATION NUMBER: US/09/875,076
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 09/417,044
PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR FILING DATE: 1999-02-16
PRIOR APPLICATION NUMBER: 60/121,851
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/123,946
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,949
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/136,436
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,437
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,439
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,567
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/137,127
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/137,131
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/141,448
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: 60/156,653
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/156,653
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/156,555
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/156,634
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/157,280
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,284
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,281
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,293
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,282
PRIOR FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
LENGTH: 390
TYPE: PRT
ORGANISM: Homo sapiens
US-09-875-076-14

Query Match      100.0%; Score 2024; DB 3; Length 390;
Best Local Similarity 100.0%; Pred. No. 1,4e-173;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Db      1  MEDNSTITLSTVTLTAFMSLVAFALMGNALVTLAEVVDKNLHRSSYFFNLAIIS 60
1  MEDNSTITLSTVTLTAFMSLVAFALMGNALVTLAEVVDKNLHRSSYFFNLAIIS 60
QY      61  DFEVGVISIPLYIPTHTLFEMDPGKICVFMLTDTYLLCTASVNIIVLISDRILSYSNAY 120
61  DFEVGVISIPLYIPTHTLFEMDPGKEICVFMLTDTYLLCTASVNIIVLISDRILSYSNAY 120
QY      121  SVRTGHTGVLKIVTLMAVWVLAEFLVNGPMLVSESKMDGSGCEPGFSEWYTLAITSP 180

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Query Match	100.0%	Score 2024	DB 3	Length 390
Best Local Similarity	100.0%	Pred. No. 1.4e-173		
Matches 390	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy	1	MPDINSTINTSLSTRVTLAFPMISVAFAMLGNALVTLAFVDDKNLRHRSYFFFLNLAIS	60	
Db	1	MPDINSTINTSLSTRVTLAFPMISVAFAMLGNALVTLAFVDDKNLRHRSYFFFLNLAIS	60	
Qy	61	DFPVGVISILPLYPHTLFEWDFGKEICVFWLTTDYLLCTASVNNIULISYRRLYSNAV	120	
Db	61	DFPVGVISILPLYPHTLFEWDFGKEICVFWLTTDYLLCTASVNNIULISYRRLYSNAV	120	
Qy	121	SYRQHGTVLKIYVILMAVAVVTLAFVLNVPMLIVSESNKDESGCEPGFFSEWYILATNSF	180	

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Db 121 SYRQHTGVLTAVTLVAVVWVLAFLVNGPMILVSSWMDSECGCPGFSEWYILATISF 180
Qy 181 LEFVPIVTLVAVFNNNTIYWSLMKRDHLSCQSHPGILTAVSSNICGHSFRGLSSRRSLA 240
Db 181 LEFVPIVTLVAVFNNNTIYWSLMKRDHLSCQSHPGILTAVSSNICGHSFRGLSSRRSLA 240
Qy 241 STEVPASFHSRORRKSLSMFSSRTKNSNTIASKMGSFQSDSVLAHQREHVELLRARR 300
Db 241 STEVPASFHSRORRKSLSMFSSRTKNSNTIASKMGSFQSDSVLAHQREHVELLRARR 300
Qy 301 LAKSLAILLGVAFCWAPYSLFTIYLSFYSSATGPKSVWYRIAFWLQWPNSEFVNPILYPL 360
Db 301 LAKSLAILLGVAFCWAPYSLFTIYLSFYSSATGPKSVWYRIAFWLQWPNSEFVNPILYPL 360
Qy 361 CHRKFOKAFKIFCIKQPLPSQHSRSVSS 390
Db 361 CHRKFOKAFKIFCIKQPLPSQHSRSVSS 390

RESULT 4
US-09-876-252-14
; Sequence 14, Application US/09876252
; Publication No. US20030018182A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Lehmann-Brulisma, Karin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Lin, I-Lin
; APPLICANT: Dang, Huong T.
; APPLICANT: Chen, Ruoping
; APPLICANT: Law, Chen W.
; TITLE OF INVENTION: Non-Endogenous Constitively Activated Human G Protein Coupled Rec
; FILE REFERENCE: AREN-0054
; CURRENT APPLICATION NUMBER: US/09/876,252
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,951
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/152,524
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/151,114
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/108,029
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
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; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-876-252-14

Query Match 100.0%; Score 2024; DB 3; Length 390;
Best Local Similarity 100.0%; Pred. No. 1,4e-173;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPDNTNSTINSLSTRVTYLAFFMSLVAFALMGNALVTLAFVVDKGLRHRSSYFFLNLAIS 60
Db 1 MPDNTNSTINSLSTRVTYLAFFMSLVAFALMGNALVTLAFVVDKGLRHRSSYFFLNLAIS 60
Qy 61 DFFGVGISIPLYIPIHLFEWDFGKEICVFWLTTDYLLCTASVYNIYLISYDRYLSVSNV 120
Db 61 DFFGVGISIPLYIPIHLFEWDFGKEICVFWLTTDYLLCTASVYNIYLISYDRYLSVSNV 120
Qy 121 SYRQHTGVLTAVTLVAVVWVLAFLVNGPMILVSESKMGESCEBPGFSEWYILATISF 180
Db 121 SYRQHTGVLTAVTLVAVVWVLAFLVNGPMILVSESKMGESCEBPGFSEWYILATISF 180
Qy 181 LEFVPIVTLVAVFNNNTIYWSLMKRDHLSCQSHPGILTAVSSNICGHSFRGLSSRRSLA 240
Db 181 LEFVPIVTLVAVFNNNTIYWSLMKRDHLSCQSHPGILTAVSSNICGHSFRGLSSRRSLA 240
Qy 241 STEVPASFHSRORRKSLSMFSSRTKNSNTIASKMGSFQSDSVLAHQREHVELLRARR 300
Db 241 STEVPASFHSRORRKSLSMFSSRTKNSNTIASKMGSFQSDSVLAHQREHVELLRARR 300
Qy 301 LAKSLAILLGVAFCWAPYSLFTIYLSFYSSATGPKSVWYRIAFWLQWPNSEFVNPILYPL 360
Db 301 LAKSLAILLGVAFCWAPYSLFTIYLSFYSSATGPKSVWYRIAFWLQWPNSEFVNPILYPL 360
Qy 361 CHRKFOKAFKIFCIKQPLPSQHSRSVSS 390
Db 361 CHRKFOKAFKIFCIKQPLPSQHSRSVSS 390

RESULT 5
US-09-852-165-2
; Sequence 2, Application US/09852165
; Publication No. US20030032784A1
; GENERAL INFORMATION:
; APPLICANT: Lind, Peter
; APPLICANT: Sejlitz, Torsten
; APPLICANT: Vogelii, Gabriel
```

APPLICANT: Wood, Linda S.
TITLE OF INVENTION: No. US20030032784A1el G Protein-Coupled Receptors
FILE REFERENCE: 00231legus
CURRENT APPLICATION NUMBER: US/09/852,165
CURRENT FILING DATE: 2001-05-08
PRIOR APPLICATION NUMBER: USSN 60/203,108
PRIOR FILING DATE: 2000-05-08
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 390
TYPE: PRT
ORGANISM: Homo sapiens
US-09-852-165-2

Query Match 100.0%; Score 2024; DB 3; Length 390;
Best Local Similarity 100.0%; Pred. No. 1,4e-173;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPDINSTINLSLSTRVTLAFMSLVAFAIMGNALVILAFVVDKNLHRSSYFFLNLAIS 60
Db 1 MPDINSTINLSLSTRVTLAFMSLVAFAIMGNALVILAFVVDKNLHRSSYFFLNLAIS 60
Qy 61 DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTTDYLLCTASVNIIVLISDRYLSVSNV 120
Db 61 DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTTDYLLCTASVNIIVLISDRYLSVSNV 120
Qy 121 SYRQHTGVAKIYTLMAVAVWLAFVNGPMILVSESWKDGSECEPGFSEMYLIATTSF 180
Db 121 SYRQHTGVAKIYTLMAVAVWLAFVNGPMILVSESWKDGSECEPGFSEMYLIATTSF 180
Qy 181 LEFVPIVILVAFNNNIYMSLMKRDHLSCQSHPGLTAVSNTICGHSFRGLSSRRSLSA 240
Db 181 LEFVPIVILVAFNNNIYMSLMKRDHLSCQSHPGLTAVSNTICGHSFRGLSSRRSLSA 240
Qy 241 STEVPASFSESRQKSLMFSSRTKNSNTIASKMGSEFQSDSVALLHOREHEVELLRAR 300
Db 241 STEVPASFSESRQKSLMFSSRTKNSNTIASKMGSEFQSDSVALLHOREHEVELLRAR 300
Qy 301 LAKSLAILLGVAFCVAPYSLFTTIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPLLYPL 360
Db 301 LAKSLAILLGVAFCVAPYSLFTTIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPLLYPL 360
Qy 361 CHKRFOKAFKIFCIKQPLPSQHSRSVSS 390
Db 361 CHKRFOKAFKIFCIKQPLPSQHSRSVSS 390

RESULT 6
US-09-891-138A-6
Sequence 6, Application US/09891138A
Publication No. US20030083245A1
GENERAL INFORMATION:
APPLICANT: Lin, Daniel Chi-Hong
APPLICANT: Zhao, Jiayang
APPLICANT: Chen, Jin-Long
APPLICANT: Cui, Gene
APPLICANT: Tularik Inc.
TITLE OF INVENTION: No. US20030083245A1el Receptors
FILE REFERENCE: 018781-006210US
CURRENT APPLICATION NUMBER: US/09/891,138A
CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: US 60/213,461
PRIOR FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 390
TYPE: PRT
ORGANISM: Homo sapiens
OTHER INFORMATION: human TGR62 G-protein coupled receptor (GPCR)
US-09-891-138A-6

Query Match 100.0%; Score 2024; DB 3; Length 390;
Best Local Similarity 100.0%; Pred. No. 1,4e-173;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPDINSTINLSLSTRVTLAFMSLVAFAIMGNALVILAFVVDKNLHRSSYFFLNLAIS 60
Db 1 MPDINSTINLSLSTRVTLAFMSLVAFAIMGNALVILAFVVDKNLHRSSYFFLNLAIS 60
Qy 61 DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTTDYLLCTASVNIIVLISDRYLSVSNV 120
Db 61 DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTTDYLLCTASVNIIVLISDRYLSVSNV 120
Qy 121 SYRQHTGVAKIYTLMAVAVWLAFVNGPMILVSESWKDGSECEPGFSEMYLIATTSF 180
Db 121 SYRQHTGVAKIYTLMAVAVWLAFVNGPMILVSESWKDGSECEPGFSEMYLIATTSF 180
Qy 181 LEFVPIVILVAFNNNIYMSLMKRDHLSCQSHPGLTAVSNTICGHSFRGLSSRRSLSA 240
Db 181 LEFVPIVILVAFNNNIYMSLMKRDHLSCQSHPGLTAVSNTICGHSFRGLSSRRSLSA 240
Qy 241 STEVPASFSESRQKSLMFSSRTKNSNTIASKMGSEFQSDSVALLHOREHEVELLRAR 300
Db 241 STEVPASFSESRQKSLMFSSRTKNSNTIASKMGSEFQSDSVALLHOREHEVELLRAR 300
Qy 301 LAKSLAILLGVAFCVAPYSLFTTIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPLLYPL 360
Db 301 LAKSLAILLGVAFCVAPYSLFTTIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPLLYPL 360
Qy 361 CHKRFOKAFKIFCIKQPLPSQHSRSVSS 390
Db 361 CHKRFOKAFKIFCIKQPLPSQHSRSVSS 390

RESULT 7
US-10-052-193-2
Sequence 2, Application US/10052193
Publication No. US20020132755A1
GENERAL INFORMATION:
APPLICANT: Pfizer, Inc.
TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
FILE REFERENCE: PCI0963A
CURRENT APPLICATION NUMBER: US/10/052,193
CURRENT FILING DATE: 2002-01-17
PRIOR APPLICATION NUMBER: 0101223.6
PRIOR FILING DATE: 2001-01-17
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 390
TYPE: PRT
ORGANISM: Homo sapiens
US-10-052-193-2

Query Match 100.0%; Score 2024; DB 4; Length 390;
Best Local Similarity 100.0%; Pred. No. 1,4e-173;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPDINSTINLSLSTRVTLAFMSLVAFAIMGNALVILAFVVDKNLHRSSYFFLNLAIS 60
Db 1 MPDINSTINLSLSTRVTLAFMSLVAFAIMGNALVILAFVVDKNLHRSSYFFLNLAIS 60
Qy 61 DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTTDYLLCTASVNIIVLISDRYLSVSNV 120
Db 61 DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTTDYLLCTASVNIIVLISDRYLSVSNV 120
Qy 121 SYRQHTGVAKIYTLMAVAVWLAFVNGPMILVSESWKDGSECEPGFSEMYLIATTSF 180
Db 121 SYRQHTGVAKIYTLMAVAVWLAFVNGPMILVSESWKDGSECEPGFSEMYLIATTSF 180
Qy 181 LEFVPIVILVAFNNNIYMSLMKRDHLSCQSHPGLTAVSNTICGHSFRGLSSRRSLSA 240
Db 181 LEFVPIVILVAFNNNIYMSLMKRDHLSCQSHPGLTAVSNTICGHSFRGLSSRRSLSA 240

Qy 241 STEVPASFSRERORRKSLSMTSSRTKMSNTTASMKGSFSQSDSVALHOREHEVELLRAR 300
Db 241 STEVPASFSRERORRKSLSMTSSRTKMSNTTASMKGSFSQSDSVALHOREHEVELLRAR 300
Qy 301 LAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSWYRIAFWLQWNSFVNPLLYPL 360
Db 301 LAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSWYRIAFWLQWNSFVNPLLYPL 360
Qy 361 CHKRFOKAFKIFCIKKOPLPSQHSRSYS 390
Db 361 CHKRFOKAFKIFCIKKOPLPSQHSRSYS 390

RESULT 8
US-10-225-567A-629

Sequence 629, Application US/10225567A
Publication No. US20030113798A1
GENERAL INFORMATION:
APPLICANT: Lifespan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burnet, Glenn C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/0/225,567A
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: PatentIn version 3.1
SEQ ID NO 629
LENGTH: 390
TYPE: PRT
ORGANISM: Homo sapiens
US-10-225-567A-629

Query Match 100.0%; Score 2024; DB 4; Length 390;
Best Local Similarity 100.0%; Pred. No. 1,4e-173;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPDNTNSTINSLSTRVTLAFMSLVAFIMLGNALVILAFVVDKMLRHRSYFFLNLAIS 60
Db 1 MPDNTNSTINSLSTRVTLAFMSLVAFIMLGNALVILAFVVDKMLRHRSYFFLNLAIS 60
Qy 61 DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTTDYLCTASVNIIVLISYDRYLSVSNV 120
Db 61 DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTTDYLCTASVNIIVLISYDRYLSVSNV 120
Qy 121 SYRTOHTGVAKITVLMAVAVLFLVNGPMILVSESWKDESGECPGFSEWYLLATTSF 180
Db 121 SYRTOHTGVAKITVLMAVAVLFLVNGPMILVSESWKDESGECPGFSEWYLLATTSF 180
Qy 121 SYRTOHTGVAKITVLMAVAVLFLVNGPMILVSESWKDESGECPGFSEWYLLATTSF 180
Db 121 SYRTOHTGVAKITVLMAVAVLFLVNGPMILVSESWKDESGECPGFSEWYLLATTSF 180
Qy 181 LEFVTPILVAAYFMNNTIYMSLMKRDHLSRCOSHGLTAVSSNICGHSFRGLSSRRSLA 240
Db 181 LEFVTPILVAAYFMNNTIYMSLMKRDHLSRCOSHGLTAVSSNICGHSFRGLSSRRSLA 240
Qy 181 LEFVTPILVAAYFMNNTIYMSLMKRDHLSRCOSHGLTAVSSNICGHSFRGLSSRRSLA 240
Db 181 LEFVTPILVAAYFMNNTIYMSLMKRDHLSRCOSHGLTAVSSNICGHSFRGLSSRRSLA 240
Qy 241 STEVPASFSRERORRKSLSMTSSRTKMSNTTASMKGSFSQSDSVALHOREHEVELLRAR 300
Db 241 STEVPASFSRERORRKSLSMTSSRTKMSNTTASMKGSFSQSDSVALHOREHEVELLRAR 300
Qy 301 LAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSWYRIAFWLQWNSFVNPLLYPL 360
Db 301 LAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSWYRIAFWLQWNSFVNPLLYPL 360
Qy 361 CHKRFOKAFKIFCIKKOPLPSQHSRSYS 390
Db 361 CHKRFOKAFKIFCIKKOPLPSQHSRSYS 390

RESULT 9
US-10-272-983-14
Sequence 14, Application US/10272983

Publication No. US20030148450A1

GENERAL INFORMATION:
APPLICANT: Chen, Kuoping
APPLICANT: Dang, Huang T.
APPLICANT: Liaw, Chen W.
APPLICANT: Lin, I-Lin
TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
FILE REFERENCE: AREN0050
CURRENT APPLICATION NUMBER: US/10/272,983
PRIOR FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: US/09/417,044
PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 60/109,213
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR FILING DATE: 1999-02-16
PRIOR APPLICATION NUMBER: 60/121,851
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/123,946
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,949
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/136,436
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,437
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,439
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,567
PRIOR FILING DATE: 1999-05-28
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 390
TYPE: PRT
ORGANISM: Homo sapiens
US-10-272-983-14

Query Match 100.0%; Score 2024; DB 4; Length 390;
Best Local Similarity 100.0%; Pred. No. 1,4e-173;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPDNTNSTINSLSTRVTLAFMSLVAFIMLGNALVILAFVVDKMLRHRSYFFLNLAIS 60
Db 1 MPDNTNSTINSLSTRVTLAFMSLVAFIMLGNALVILAFVVDKMLRHRSYFFLNLAIS 60
Qy 61 DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTTDYLCTASVNIIVLISYDRYLSVSNV 120
Db 61 DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTTDYLCTASVNIIVLISYDRYLSVSNV 120
Qy 121 SYRTOHTGVAKITVLMAVAVLFLVNGPMILVSESWKDESGECPGFSEWYLLATTSF 180
Db 121 SYRTOHTGVAKITVLMAVAVLFLVNGPMILVSESWKDESGECPGFSEWYLLATTSF 180
Qy 121 SYRTOHTGVAKITVLMAVAVLFLVNGPMILVSESWKDESGECPGFSEWYLLATTSF 180
Db 121 SYRTOHTGVAKITVLMAVAVLFLVNGPMILVSESWKDESGECPGFSEWYLLATTSF 180
Qy 181 LEFVTPILVAAYFMNNTIYMSLMKRDHLSRCOSHGLTAVSSNICGHSFRGLSSRRSLA 240
Db 181 LEFVTPILVAAYFMNNTIYMSLMKRDHLSRCOSHGLTAVSSNICGHSFRGLSSRRSLA 240
Qy 181 LEFVTPILVAAYFMNNTIYMSLMKRDHLSRCOSHGLTAVSSNICGHSFRGLSSRRSLA 240
Db 181 LEFVTPILVAAYFMNNTIYMSLMKRDHLSRCOSHGLTAVSSNICGHSFRGLSSRRSLA 240
Qy 241 STEVPASFSRERORRKSLSMTSSRTKMSNTTASMKGSFSQSDSVALHOREHEVELLRAR 300
Db 241 STEVPASFSRERORRKSLSMTSSRTKMSNTTASMKGSFSQSDSVALHOREHEVELLRAR 300
Qy 301 LAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSWYRIAFWLQWNSFVNPLLYPL 360
Db 301 LAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSWYRIAFWLQWNSFVNPLLYPL 360
Qy 361 CHKRFOKAFKIFCIKKOPLPSQHSRSYS 390
Db 361 CHKRFOKAFKIFCIKKOPLPSQHSRSYS 390

RESULT 10


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US-10-354-769-2
; Sequence 2, Application US/10354769
; Publication No. US20030149242A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: O'Reilly, Mark A.
; TITLE OF INVENTION: NOVEL POLYPEPTIDE
; FILE REFERENCE: PCI0373B
; CURRENT APPLICATION NUMBER: US/10/354,769
; PRIOR FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 09/698,801
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/211,243
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: GB 9925641.4
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: GB 0009973.9
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-354-769-2

Query Match      100.0%; Score 2024; DB 4; Length 390;
Best Local Similarity 100.0%; Pred. No. 1.4e-173;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 MPDNTSTINLSSTRVTLAFPMSLVAFAMLGNALVILAFVVDKNLRHRSYFFFLNLAIS 60
Db 1 MPDNTSTINLSSTRVTLAFPMSLVAFAMLGNALVILAFVVDKNLRHRSYFFFLNLAIS 60
Cy 61 DFFGVGISIPLYIPIHTLFEWDGKEICVFWLTTDYLCTASVYNIVLISDYRYSVSNAY 120
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Cy 121 SYRTOHGVLTQVTLVAVVAVVLAFLVNGPMILVSESKDESGCEPGFSEMYILATISF 180
Db 121 SYRTOHGVLTQVTLVAVVAVVLAFLVNGPMILVSESKDESGCEPGFSEMYILATISF 180
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Cy 361 CHKRFOKAFKIFCIKQPLPSQHSRSVSS 390
Db 361 CHKRFOKAFKIFCIKQPLPSQHSRSVSS 390

RESULT 11
US-10-393-807-14
; Sequence 14, Application US/10393807
; Publication No. US20030175891A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huang T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/393,807
; CURRENT FILING DATE: 2003-03-21

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; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-393-807-14

Query Match      100.0%; Score 2024; DB 4; Length 390;
Best Local Similarity 100.0%; Pred. No. 1.4e-173;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MPDNTSTINLSSTRVTLAFPMSLVAFAMLGNALVILAFVVDKNLRHRSYFFFLNLAIS 60
Cy 61 DFFGVGISIPLYIPIHTLFEWDGKEICVFWLTTDYLCTASVYNIVLISDYRYSVSNAY 120
Db 61 DFFGVGISIPLYIPIHTLFEWDGKEICVFWLTTDYLCTASVYNIVLISDYRYSVSNAY 120
Cy 121 SYRTOHGVLTQVTLVAVVAVVLAFLVNGPMILVSESKDESGCEPGFSEMYILATISF 180
Db 121 SYRTOHGVLTQVTLVAVVAVVLAFLVNGPMILVSESKDESGCEPGFSEMYILATISF 180
Cy 181 LEFVPIVLVAVFNNNIYMSLMKRDHLSRCQSHPGLTAVSNI CGHSFRGLSSRRSISA 240
Db 181 LEFVPIVLVAVFNNNIYMSLMKRDHLSRCQSHPGLTAVSNI CGHSFRGLSSRRSISA 240
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Db 241 STEVPASHSESRQRKSSLMFSSRTKNSNTIASKMGSPQSDVALHOREHVELLRAR 300
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Db 361 CHKRFOKAFKIFCIKQPLPSQHSRSVSS 390

RESULT 12
US-10-417-820A-14
; Sequence 14, Application US/10417820A
; Publication No. US20030229216A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lowitz, Kevin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Behan, Dominic P.
; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled

```

TITLE OF INVENTION: Receptors
FILE REFERENCE: 7.US28.CON
CURRENT APPLICATION NUMBER: US/10/417,820A
CURRENT FILING DATE: 2003-04-16
PRIOR APPLICATION NUMBER: 09/416,760
PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: 60/110,060
PRIOR FILING DATE: 1998-11-27
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR FILING DATE: 1999-02-16
PRIOR APPLICATION NUMBER: 60/121,852
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/109,213
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: 60/123,944
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,945
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,948
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,951
PRIOR FILING DATE: 1999-03-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 155
SOFTWARE: Patent version 3.2
SEQ ID NO 14
LENGTH: 390
TYPE: PRT
ORGANISM: Homo sapiens
US-10-417-820A-14

Query Match 100.0%; Score 2024; DB 4; Length 390;
Best Local Similarity 100.0%; Pred. No. 1,4e-173;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 DFFGVGISIPYIPIHTLFEMDPGKEICVFWLTTDYLCTASVYVILSYDRYLSVSNV 120
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DB 361 CHKRFOKAFKIFCTIKQPLPSQHSRSVSS 390

RESULT 13
US-10-349-253A-2
Sequence 2, Application US/10349253A
Publication No. US2004004393A1
GENERAL INFORMATION:
APPLICANT: Aubart, Kelly
APPLICANT: Bergema, Dirk

APPLICANT: Fitzgerald, Laura
APPLICANT: Graybill, Todd
APPLICANT: Li, Xiaolong
APPLICANT: Michalovich, David
APPLICANT: Morrow, Dwight
APPLICANT: Zhu, Yuan
TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor
FILE REFERENCE: GP70655-2C2
CURRENT APPLICATION NUMBER: US/10/349,253A
CURRENT FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: 09/910,411
PRIOR FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: 09/693,761
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 09/497,790
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/431,898
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 390
TYPE: PRT
ORGANISM: Homo sapien
US-10-349-253A-2

Query Match 100.0%; Score 2024; DB 4; Length 390;
Best Local Similarity 100.0%; Pred. No. 1,4e-173;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 361 CHKRFOKAFKIFCTIKQPLPSQHSRSVSS 390

RESULT 14
US-10-636-673-2
Sequence 2, Application US/10696673
Publication No. US20040105846A1
GENERAL INFORMATION:
APPLICANT: Pharmacia & Upjohn Company
APPLICANT: Lind, Peter
APPLICANT: Sejlitz, Torsten
APPLICANT: Vogeli, Gabriel
APPLICANT: Wood, Linda S
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: PHRM0025-101/00231REGUS.1.DV1
CURRENT APPLICATION NUMBER: US/10/696,673
CURRENT FILING DATE: 2003-10-28

PRIOR APPLICATION NUMBER: US 60/203,108
PRIOR FILING DATE: 2000-05-08
PRIOR APPLICATION NUMBER: US 09/852,165
PRIOR FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 390
TYPE: PRT
ORGANISM: Homo sapiens
US-10-696-673-2

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DB 361 CHKRFQAKFLKIFCIKQPLPSOHSRSVSS 390

RESULT 15

US-10-723-955-14
Sequence 14, Application US/10723955
Publication No. US20040110238A1
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Lin, I-tin
APPLICANT: Liaw, Chen W.
APPLICANT: Lehman-Brunsmma, Karin
APPLICANT: Lowitz, Kevin P.
APPLICANT: Dang, Huang T.
APPLICANT: Chen, Ruoping
APPLICANT: Gore, Martin
APPLICANT: White, Carol
TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
FILE REFERENCE: 7.US29.CON
CURRENT APPLICATION NUMBER: US/10/723,955
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 10/417,820
PRIOR FILING DATE: 2003-4-16
PRIOR APPLICATION NUMBER: 09/416,760
PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: 60/110,060
PRIOR FILING DATE: 1998-11-27

PRIOR APPLICATION NUMBER: 60/120,416
PRIOR FILING DATE: 1999-02-16
PRIOR APPLICATION NUMBER: 60/121,852
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/109,213
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: 60/123,944
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,945
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,948
PRIOR FILING DATE: 1999-03-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 148
SOFTWARE: PatentIn version 3.2
SEQ ID NO 14
LENGTH: 390
TYPE: PRT
ORGANISM: Homo sapiens
US-10-723-955-14

Query Match 100.0%; Score 2024; DB 4; Length 390;
Best Local Similarity 100.0%; Pred. No. 1,4e-173;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 361 CHKRFQAKFLKIFCIKQPLPSOHSRSVSS 390

Search completed: March 28, 2006, 14:03:02
Job time: 167 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 28, 2006, 14:00:25 ; Search time 24 Seconds
(without alignments)
479.284 Million cell updates/sec

Title: US-10-616-088-2

Perfect score: 2024
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Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 174695 seqs, 29494374 residues

Total number of hits satisfying chosen parameters: 174695

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:*

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2: /SIDS/prodata/1/pubppaa/US06_NEW_PUB.pep:*
3: /SIDS/prodata/1/pubppaa/US07_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	772	38.1	441	7	US-11-241-956-3 Sequence 3, Appli
2	730	36.1	445	7	US-11-115-564-2 Sequence 2, Appli
3	729	36.0	445	7	US-11-115-564-3 Sequence 3, Appli
4	724	35.8	445	7	US-11-115-564-1 Sequence 1, Appli
5	411	20.3	590	7	US-11-124-368A-183 Sequence 183, App
6	411	20.3	590	7	US-11-127-877-54 Sequence 54, Appl
7	397.5	19.6	532	7	US-11-127-877-42 Sequence 42, Appl
8	386	19.1	466	7	US-11-127-877-41 Sequence 41, Appl
9	384.5	19.0	480	6	US-10-521-162-40 Sequence 40, Appl
10	377.5	18.7	429	7	US-11-127-877-51 Sequence 51, Appl
11	377.5	18.7	466	7	US-11-127-877-50 Sequence 50, Appl
12	375	18.5	353	6	US-10-875-716-10 Sequence 10, Appl
13	372	18.4	487	7	US-11-248-847-582 Sequence 582, App
14	348.5	17.2	400	6	US-10-499-210-2 Sequence 2, Appli
15	344	17.0	350	7	US-11-165-024-3 Sequence 3, Appli
16	314.5	15.5	446	7	US-11-166-412-67 Sequence 67, Appli
17	314	15.5	345	7	US-11-174-816-15 Sequence 15, Appl
18	314	15.5	345	7	US-11-174-819-70 Sequence 70, Appl
19	313	15.5	712	6	US-10-521-162-12 Sequence 12, Appl
20	310	15.3	365	6	US-10-875-716-9 Sequence 9, Appli
21	300.5	14.8	475	6	US-10-877-346-48 Sequence 48, Appl
22	299.5	14.7	345	7	US-11-174-751-16 Sequence 16, Appl
23	298	14.7	345	7	US-11-174-816-59 Sequence 59, Appl
24	296	14.6	345	7	US-11-174-819-78 Sequence 78, Appl
25	296	14.6	345	7	US-11-174-816-44 Sequence 44, Appl

26	296	14.6	345	7	US-11-174-819-13 Sequence 13, Appl
27	294.5	14.6	471	6	US-10-995-561-901 Sequence 901, App
28	291	14.4	348	7	US-11-174-751-12 Sequence 12, Appl
29	288	14.2	269	7	US-11-151-482-5 Sequence 5, Appli
30	285	14.1	477	6	US-10-877-346-47 Sequence 47, Appl
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32	282.5	14.0	347	7	US-11-174-819-76 Sequence 76, Appl
33	282	13.9	457	6	US-10-877-346-49 Sequence 49, Appl
34	281.5	13.9	347	7	US-11-174-816-42 Sequence 42, Appl
35	281.5	13.9	347	7	US-11-174-819-9 Sequence 9, Appli
36	280	13.8	458	6	US-10-877-346-51 Sequence 51, Appl
37	279.5	13.8	332	7	US-11-174-816-39 Sequence 39, Appl
38	279.5	13.8	332	7	US-11-174-819-3 Sequence 3, Appli
39	279.5	13.8	349	7	US-11-174-751-22 Sequence 22, Appl
40	278.5	13.8	440	6	US-10-502-893-2 Sequence 2, Appli
41	275	13.6	348	7	US-11-174-816-11 Sequence 11, Appl
42	275	13.6	348	7	US-11-174-816-48 Sequence 48, Appl
43	275	13.6	348	7	US-11-174-819-14 Sequence 34, Appl
44	274.5	13.6	481	7	US-11-090-439-16 Sequence 16, Appl
45	274.5	13.6	486	6	US-10-877-346-50 Sequence 50, Appl

ALIGNMENTS

RESULT 1
US-11-241-956-3
Sequence 3, Application US/11241956
Publication No. US20060024792A1
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS INC.; BAUGHN, Mariah R.;
APPLICANT: GRANT, Richard C.; CHAMLA, Nardinder K.;
APPLICANT: GARDHI, Ameena R.; HAPFLIN, April J.A.;
APPLICANT: RAMKUMAR, Jayalaxmi; TRIBOLET, Catherine M.;
APPLICANT: THORNTON, Michael B.; KALIRICK, Deborah A.;
APPLICANT: YAO, Monique G.; ELLIOTT, Vicki S.;
APPLICANT: BURFORD, Neil; KHAN, Farrah A.;
APPLICANT: YUE, Henry; LU, Yant; ROOPA, Reddy M.;
APPLICANT: ARVIZU, Chandra S.; LEE, Ernestine A.;
APPLICANT: NGUYEN, Daniel B.; LEE, Ernestine A.;
APPLICANT: LU, Dying Anna M.; ISON, Craig H.;
APPLICANT: WALSH, Roderick T.; POLICKY, Jennifer L.
TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
FILE REFERENCE: PI-0236 USN
CURRENT APPLICATION NUMBER: US/11/241,956
PRIOR APPLICATION NUMBER: US/10/398,036
PRIOR FILING DATE: 2003-03-28
PRIOR APPLICATION NUMBER: PCT/US01/30661
PRIOR FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US 60/245,855
PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: US 60/242,322
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/240,589
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: US 60/249,343
PRIOR FILING DATE: 2000-11-15
PRIOR APPLICATION NUMBER: US 60/247,587
PRIOR FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: US 60/245,900
PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: US 60/242,223
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: US 60/236,546
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ. ID NOS: 32
SOFTWARE: PERL Program
SEQ. ID NO 3
LENGTH: 441
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:

NAME/KEY: misc:feature
OTHER INFORMATION: incyte ID No: 7474823CD1
US-11-956-3

Query Match 38.1%; Score 772; DB 7; Length 441;

Best Local Similarity 62.1%; Pred. No. 3.5e-61; Mismatches 43; Indels 34; Gaps 8;

Matches 167; Conservative 25; Mismatches 43; Indels 34; Gaps 8;

57 LAISDFE---VGVISIPLYIPHTLFEWDFGKEICVFWLTTDYLLCTASVYNIYLISYDR 112
106 LEVDFTEVTOQSVISIPLYIPHTLFEWDFGKEICVFWLTTDYLLCTASVYNIYLISYDR 165
113 YLSVSNVSYRTORTGVKITYTLMAVAVVLAFLVNGPMILVSESKDGSCEGPFSEW 172
166 YLSVSNVSYRTORTGVKITYTLMAVAVVLAFLVNGPMILVSESKDGSCEGPFSEW 225
173 YLIAITSLFEVPIVILVAVFNNIYVSLMKRDHLSCQSHPG---LTVASSNICHS 227
226 YLIAITSLFEVPIVILVAVFNNIYVSLMKRDHLR--LGHFKMGOLVLRPHGVGQP 283
228 FRGLSSRSLASTEVASPHSERORRKSLSMFSSRTKNSNTIASK-MGSFQSDSVA 286
284 WRQL-----VPRMGYTE---VGGILCTAAGEMSTHARSAXLSTGSENDTLP 328
287 LHOREVELLPARKLASLAILLGVFANC 315
329 -----VPSLASRSLCPSEV-LSLGSFPSC 350

RESULT 2

US-11-564-2

Sequence 2, Application US/11115564

Publication No. US20050267116A1

GENERAL INFORMATION:

APPLICANT: Peschke, Bernd

APPLICANT: Hohweg, Rolf

TITLE OF INVENTION: SUBSTITUTED HEXAHYDROPYRROLO[1,2-A]PYRAZINES,

TITLE OF INVENTION: OCTAHYDROPYRIDO[1,2-A]PYRAZINES AND

TITLE OF INVENTION: DECAHYDROPIRAZINO[1,2-A]AZEPINES

FILE REFERENCE: 6483.200-US

CURRENT APPLICATION NUMBER: US/11/115,564

CURRENT FILING DATE: 2005-04-27

PRIOR APPLICATION NUMBER: US 60/387,047

PRIOR FILING DATE: 2002-06-07

PRIOR APPLICATION NUMBER: Danish Application no. PA 2002 00863

PRIOR FILING DATE: 2002-06-06

NUMBER OF SEQ ID NOS: 3

SOFTWARE: PatentIn version 3.2

SEQ ID NO 2

LENGTH: 445

TYPE: PRT

ORGANISM: Monkey

US-11-564-2

Query Match 36.1%; Score 730; DB 7; Length 445;

Best Local Similarity 39.2%; Pred. No. 1.9e-57;

Matches 168; Conservative 47; Mismatches 132; Indels 82; Gaps 10;

11 SLSTRVTLAFPMISIVAFAMIGNALVILAFVVDKRLRRSSYFPLNALISDPFVGVISIP 70
30 SAAMTAVLALMALIYATVIGNALVILAFVADSSLRTONNFFLNALISDPVGAFCIP 89
71 LYIPHTLE-EMDFGKEICVFWLTTDYLLCTASVYNIYLISYDRYLSVSNVSYRTORTGV 129
90 LYVPYVLGRWTFGRGLCKLMLVDYLLCTSSAFNIVILISYDRFLSVTRAVSYRAOQDNT 149
130 LKIVTLMAVAVVLAFLVNGPMILVSESK-----DEGSECEGPFSEWYLIAITSL 181
150 RRAVKRMLVAVVLAFLVNGPMILVSESK-----SWEYLSGSSSIPEG-HCYAEFFYNNYFLITASTL 205
182 EFVIFVILVAVFNNIY-----NSLMKRD 205
206 EFTFPLSVTFNNISYLTNTQRTRLDLGAREAGPPEPPAOPSPPPPCGCMCKG 265

206 HLSRCQSH-----PGLTAVSNICGHSFRGRSLSRRLSASTEVPAFHSERQ 253
266 HGEAMPLHRYGVGEAAGAGETALGGGGGSAASPTSSGSSRGTFRPPSLKRGSK 325
254 RRKSSLSMFSSRTKNSNTIASKMGSPQSDSVALLHOREVELLPARKLASLAILLGVFA 313
326 PSASSASLEGRMKVNSQ-----SFTQ-----RFLSRDRKVAKSLAVISIFG 368
314 VCAAPSLFTIVLSFYSSATGPKSVWYRIAFWLOFNSFVNPILLYPCHKRFQAFKIF 373
369 LCAAPYTLIMIIIRAACHGCHCP-DYWTETSPWILMANAVNPVLYPLCHHSFRALFKL 427
374 C---IKKOP 379
428 CPQKLTQIP 436

RESULT 3

US-11-564-3

Sequence 3, Application US/11115564

Publication No. US20050267116A1

GENERAL INFORMATION:

APPLICANT: Peschke, Bernd

APPLICANT: Hohweg, Rolf

TITLE OF INVENTION: SUBSTITUTED HEXAHYDROPYRROLO[1,2-A]PYRAZINES,

TITLE OF INVENTION: OCTAHYDROPYRIDO[1,2-A]PYRAZINES AND

TITLE OF INVENTION: DECAHYDROPIRAZINO[1,2-A]AZEPINES

FILE REFERENCE: 6483.200-US

CURRENT APPLICATION NUMBER: US/11/115,564

CURRENT FILING DATE: 2005-04-27

PRIOR APPLICATION NUMBER: US 60/387,047

PRIOR FILING DATE: 2002-06-07

PRIOR APPLICATION NUMBER: Danish Application no. PA 2002 00863

PRIOR FILING DATE: 2002-06-06

NUMBER OF SEQ ID NOS: 3

SOFTWARE: PatentIn version 3.2

SEQ ID NO 3

LENGTH: 445

TYPE: PRT

ORGANISM: Rat

US-11-564-3

Query Match 36.0%; Score 729; DB 7; Length 445;

Best Local Similarity 39.1%; Pred. No. 2.4e-57; Mismatches 131; Indels 74; Gaps 10;

Matches 166; Conservative 54; Mismatches 131; Indels 74; Gaps 10;

11 SLSTRVTLAFPMISIVAFAMIGNALVILAFVVDKRLRRSSYFPLNALISDPFVGVISIP 70
30 SAAMTAVLALMALIYATVIGNALVILAFVADSSLRTONNFFLNALISDPVGAFCIP 89
71 LYIPHTLE-EMDFGKEICVFWLTTDYLLCTASVYNIYLISYDRYLSVSNVSYRTORTGV 129
90 LYVPYVLGRWTFGRGLCKLMLVDYLLCTSSAFNIVILISYDRFLSVTRAVSYRAOQDNT 149
130 LKIVTLMAVAVVLAFLVNGPMILVSESK-----DEGSECEGPFSEWYLIAITSL 181
150 RRAVKRMLVAVVLAFLVNGPMILVSESK-----SWEYLSGSSSIPEG-HCYAEFFYNNYFLITASTL 205
182 EFVIFVILVAVFNNIY-----NSLMKRD 205
206 EFTFPLSVTFNNISYLTNTQRTRLDLGAREAGPPEPPAOPSPPPPCGCMCKG 265
206 HLSRCQSH-----PGLTAVSNICGHSFRGRSLSRRLSASTEVPAFHSERQ 253
266 HGEAMPLHRYGVGEAAGAGETALGGGGGSAASPTSSGSSRGTFRPPSLKRGSK 325
254 RRKSSLSMFSSRTKNSNTIASKMGSPQSDSVALLHOREVELLPARKLASLAILLGVFA 313
326 PSASSASLEGRMKVNSQ-----SFTQ-----RFLSRDRKVAKSLAVISIFG 368
314 VCAAPSLFTIVLSFYSSATGPKSVWYRIAFWLOFNSFVNPILLYPCHKRFQAFKIF 373
369 LCAAPYTLIMIIIRAACHGCHCP-DYWTETSPWILMANAVNPVLYPLCHHSFRALFKL 427
374 C---IKKOP 379
428 CPQKLTQIP 436

Db	373	PYTLIMIRACHGRGRCIP-DYMETISFWLLMANSVNPVLYPLCHVSFRRAFTKLLCPQK	433
QY	375	IKKOP	379
Db	432	LKKOP	436
<p>RESULT 4</p> <p>US-11-115-564-1</p> <p>Sequence 1, Application US/11115564</p> <p>Publication No. US20050267116A1</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Hohlweg, Bernd</p> <p>TITLE OF INVENTION: SUBSTITUTED HEXAHYDROPYRROLO[1,2-A]PYRAZINES,</p> <p>TITLE OF INVENTION: OCTAHYDROPHRIDO[1,2-A]PYRAZINES AND</p> <p>FILE REFERENCE: 6483.200-US</p> <p>CURRENT APPLICATION NUMBER: US/11/115,564</p> <p>PRIOR FILING DATE: 2005-04-27</p> <p>PRIOR APPLICATION NUMBER: US 60/387,047</p> <p>PRIOR FILING DATE: 2002-06-07</p> <p>PRIOR APPLICATION NUMBER: Danish Application no. PA 2002 00863</p> <p>PRIOR FILING DATE: 2002-06-06</p> <p>NUMBER OF SEQ ID NOS: 3</p> <p>SOFTWARE: PatentIn version 3.2</p> <p>SEQ ID NO 1</p> <p>LENGTH: 445</p> <p>TYPE: PRT</p> <p>ORGANISM: Homo Sapiens</p> <p>US-11-115-564-1</p>			
<p>Query Match 35.8%; Score 724; DB 7; Length 445;</p> <p>Best Local Similarity 38.6%; Pred. No. 6.6e-57;</p> <p>Matches 164; Conservative 56; Mismatches 131; Indels 74; Gaps 10;</p>			
QY	11	SLSTRVTLAFMSLVAFAMGNALVILLAFVVDKRLRRSSVEFLNALISDFVGVISIP	70
Db	30	SAATRAVVALMALTLIVATVFLVGNALVMLAFVADSSLRTQNNFFLNLISDFVGAFCTP	89
QY	71	LYIPHTLE-EMDFGKEICVFWLTTDYLLCTASVNIIVLISYDRYLSVSNASVYRTOHTGV	129
Db	90	LYVEYVLVGRWTFEGGLCKLMLVNDYLLCTSAFIVLISYDRFLSTRAVSYRAQOGDT	149
QY	130	LKIIVLVAVAVLAEVLVNGPMILVSESXK-----DEGSECEBGFSEWYIILATSFL	181
Db	150	RRAVRKMLVWVLAFLVGLYPAIL---SWEVLSGSSSIPDG-HCYAEFFYNNYFLITASTL	205
QY	182	EFVLPVILVAFENNNIY-----NSLMKRD	205
Db	206	EFEPFPLSVTFEFLNISLYNIORRTLRLDGAREAGPPPEAPDPSPPPPGCGCWCXKG	265
QY	206	HLSCRQSH-----PGLTAVSNICGHSFGRSLRSRSLASTREVPASFSEQRORRS	257
Db	266	HGEAMPLHRYVGAEAVAGEAEATLGGGGGGSVASPTSSGSS-----SRGTERPR	318
QY	258	SLMESSRTKNSNTIASKXGFSFQSDSVALHQREHVELLRARLAKSLAILLGVAVCWA	317
Db	319	SLKRGSKPSASASASLEKRMKVVSGFT-----QRFRLSRDRKVAKSLAIVISIFGLCWA	372
QY	318	PYSLEPTVILASYSASATGPKSVMYRIRAFMLQFNSSVNPVNLPLPLCHKRQKAFKIFC--	374
Db	373	PYTLIMIRACHGHCVP-DYMETISFWLLMANSVNPVLYPLCHVSFRRAFTKLLCPQK	431
QY	375	IKKOP	379
Db	432	LKKOP	436
<p>RESULT 5</p> <p>US-11-124-368A-183</p> <p>Sequence 183, Application US/11124368A</p> <p>Publication No. US20050287559A1</p>			

: GENERAL INFORMATION:
 : APPLICANT: Michele Cargill
 : APPLICANT: James J. Devlin
 : APPLICANT: May Luke
 : TITLE OF INVENTION: Genetic Polymorphisms Associated with
 : TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
 : FILE REFERENCE: CL001524
 : CURRENT APPLICATION NUMBER: US/11/124,368A
 : CURRENT FILING DATE: 2005-05-09
 : PRIOR APPLICATION NUMBER: US 60/569,845
 : PRIOR FILING DATE: 2004-05-07
 : PRIOR APPLICATION NUMBER: US 60/625,936
 : PRIOR FILING DATE: 2004-11-09
 : NUMBER OF SEQ. ID NOS: 21112
 : SOFTWARE: FASTSEQ for windows Version 4.0
 : SEQ ID NO 183
 : LENGTH: 590
 : TYPE: PRT
 : ORGANISM: Homo sapiens
 : US-11-124-368A-183

Query Match 20.3%; Score 411; DB 7; Length 590;
 Best Local Similarity 22.6%; Pred. No. 6,9e-29;
 Matches 118; Conservative 95; Mismatches 150; Indels 158; Gaps 14;

QY 16 VTLAFMSLVAPAFIMGNALVTLLAPVDKNNLRHSSYFELMLAISDFVGVISIPLYPH 75
 DB 69 VFPAFTGLTALVTIIGNLIVISFRVKNQKLTNNRIFLLSLACADLLIIGVISNNLFTTY 128
 QY 76 TLF-EMDFEKEICVFMLTDTDYLLCTASVYNNIVLISYDEYLSVSNASVYRTOHTGVLIKT 134
 DB 129 IINRRALGNLACDMLALDIDVYASNAVNNLIVISFDYFSTIRLTLYRAKRT--TKAG 186
 QY 135 LMVAV-VTLAPLVNGMIIIVSSSKDEGS---ECPEGFSEWYTLAITSFLEYIYPIYL 189
 DB 187 VMIGLAWVISFVLMAPALIFMQYFVGKRTVPGECFIQFLSEPTTFGTALAAFYMPVTI 246
 QY 190 VAFENNTIYSLMK----- 203
 DB 247 MTI---LVMRIYKETEKTKELAGLQASGTEAETENFVHPTGSSRSGSYELQOOSMKR 302
 QY 204 --RDHLSRC-----QSHPLGLTAVSN----- 222
 DB 303 SNRRKIKGRCHFPTTKSKMPSSEQNDQDHSSSDSMNNNDAAASLENSASDDEEDIGSTR 362
 QY 223 -----ICGHSF-----RGLSSRSLSASTEVA 246
 DB 363 AIYSIVLKLPGHSTTLINSLTKLPSNDLQVPEELGMVDLERKADKLQAKSVDOGGSFPK 422
 QY 247 SFHSERQRRKSSLSMFSRTQNSN-----TASKMGSGQSDVALHORE 291
 DB 423 SFSEKLPQLQESAVDPAKTSIDVNSVGKSTATLPLSFKEATYLAKRFLALTRFSO---ITGRK 479
 QY 292 HVEILBARLBSLAILLGVFAVCAPSLFTIYVSPFSASATGPGRSVYVYRLAFLMOWENS 351
 DB 480 RNSLVEKRAAQTLLSLIILAFITITWTFNNIMVAVTFDCSCI-PFTW-NIGIMLCYINS 537
 QY 352 FVNPFLYPLCHRRFQKAFLEKTF---CIKKOPLPSGHSRVS 389
 DB 538 TVNPVCYALCNKTFRTTFMGLLCCQDKKGRKQYQGRQS 578

RESULT 6
 US-11-127-877-54
 : Sequence 54, Application US/11127877
 : Publication No. US20050287565A1
 : GENERAL INFORMATION:
 : APPLICANT: Merchiers, Pascal G.
 : APPLICANT: Hoffmann, Marcel
 : APPLICANT: Spittaels, Koenraad F. F.
 : APPLICANT: Laenen, Wendy
 : TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
 : TITLE OF INVENTION: Amyloid-Beta Protein Production

```

? FILE REFERENCE: P27,800-B USA
? CURRENT APPLICATION NUMBER: US/11/127,877
? CURRENT FILING DATE: 2005-05-12
? PRIOR APPLICATION NUMBER: 60/570,352
? PRIOR FILING DATE: 2004-05-12
? PRIOR APPLICATION NUMBER: 60/603,948
? PRIOR FILING DATE: 2004-08-24
? NUMBER OF SEQ ID NOS: 590
? SOFTWARE: PatentIn version 3.3
? SEQ ID NO: 54
? LENGTH: 590
? TYPE: prt
? ORGANISM: Homo sapiens
?
US-11-127-877-54

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[illegible]

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; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 42
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-127-877-42

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Query Match      19.6%; Score 397.5; DB 7; Length 532;
Best Local Similarity 22.6%; Pred. No. 9.7e-28;
Matches 110; Conservative 90; Mismatches 155; Indels 131; Gaps 14,

Oy   . VTLAFMSLVAPALMGNALVITLAFVDYDKILRRSSIFFLNALAISDFVGYSIPLYPH 75
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
31 ITIAVAIVAVSLITIGVAVLMISFKINSQIKTVNNYYLLSLACADILIGIFSNNLYTYT 90
Oy   76 TLF-EPMFGKEICVPWLTDTYLCTASVYNVLISYRYSVSNAVSRYTOHTGVLKVT 134
Db   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
91 ILMGRMALGSLACDMLALDDVASNASVMNLDVISFDRYSITRPITYRAKTP--KRAG 148
Oy   135 LNVAV-VTLAFLVNGPMLIVSESWKDEGS---ECEPGFSEMYIILAITSFLEVIPVYL 189
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
149 IMIGLAMLISFILMAPAILCMQYLGKRTVPLEDCCIQFISEPTITGTALAAFYIPSV 208
Oy   190 VAYENNVIY----- 198
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
209 MTLYKRIYETEKRTDLADLGSDSVTKAEKKRPAHARLRCLRCPRITLAQRERNQ 268
Oy   199 --NSL-----W-KRDHLSCQHPC-----LTAV 219
Db   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
269 ASNWSSRSSTSTTGKPSQATGPSANMAKAQLTTCSYSYPSEDEDKPATDPVLQVYKSQ 328
Oy   220 SSNIKGHSFGRRLSSRSSLSASTE-----VASFSHEQRKRSIMFSSTRTON 268
Db   329 GKSPGEFEFAEETEFTVKARETEKSYDTPNYLLSPAHRPKSQCKVAIKFLVYKAD 388
Oy   269 SN-----TIASMGCS-FSOSDSVALHOREHELLRARLARSLATILL 309
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
389 GNQGTNNCGHKAKIMPCFPVPAWEPTSKGNLPNSHQMTARKRVLVKERRQAQTLSAIL 448
Oy   310 GVPAVCAPAYSLETTIVLSFYSSATGPKSVWYRIAFLWMQENSFVNPLIPLYCHKRFQCAF 369
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
449 LAFITTPINIMVLGSTFCOKCV-PYTLMH-LGYMLCYVNSTVNPICYALCNRTFRKTF 506
Oy   370 -LKIFC 374
Db   : : : : :
507 KMLILC 512

RESULT 8
US-11-127-877-41
: Sequence 41, Application US/11127877
: Publication No. US20050287565A1
GENERAL INFORMATION:
APPLICANT: Merchiers, Pascal G.
APPLICANT: Hoffmann, Marcel
APPLICANT: Spittelaes, Koenaad F. F.
APPLICANT: Laenen, Wendy
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
FILE OF INVENTION: Amyloid-Beta Protein Production
FILE REFERENCE: P27,800-B USA
CURRENT APPLICATION NUMBER: US/11/127,877
CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: 60/570,352
PRIOR FILING DATE: 2004-05-12
PRIOR APPLICATION NUMBER: 60/603,948
PRIOR FILING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 590
SOFTWARE: PatentIn version 3.3
SEQ ID NO 41
LENGTH: 466
TYPE: PRt
```


ORGANISM: Homo sapiens
US-11-127-877-41

Query Match 19.1%; Score 386; DB 7; Length 466;
Best Local Similarity 24.1%; Pred. No. 8.8e-27;
Matches 110; Conservative 96; Mismatches 147; Indels 104; Gaps 17;

QX 4 TNSTNLSTLRVTLAFFMSLVAFAI---MGNALVLAFAVVDKNLRHRSYFELNLA1 59
DB 8 SNNLSLTPYKTEFEVFLVAGSLSLVTITGNLWMSIVNHLQTVNNYFLPSLAC 67
QY 60 SDFEFGVSIPLYPHTLF-EWDFGKEICFVMTLDYLLCTASVYNYLISYDRILSYSN 118
DB 68 ADLIIGVFSMLYLYTYIGVWPLGPVCDLMLADYVSNASVNNLLISDRFCYTK 127
QY 119 AVSRTQHTGVKIVTLNV-AVWLAFLVNGMILVSSWK-----DESGCEGPFPS 170
DB 128 PLTYPVKRT--TKMGMMIAAAWVLSFILMAFALF---WQPIVGVRTVEDECYIOFSS 182
QY 171 EMTYLAITSFLEFVPIVLAFAFMNNTYWSLMK--RDHLSCQSHPGGLTAVSNICGHSF 228
DB 183 NAAVTFGTAIAFLYLPVIMTV---LYWHISRAKSRKIKDKKEP--VANODPVPSPLV 236
QY 229 RGRL-----HSEQRKRS-LMSSRTKMN---SNTIASKGSGFSQS--D 283
DB 237 QGRIVKPNNNMPPSSDGLHNKIKNGKAPDPTVENCVOGEKSSNDSTSVSAVSNM 296
QY 249 -----HSEQRKRS-LMSSRTKMN---SNTIASKGSGFSQS--D 283
DB 297 RDEITQDENTVSTGSKDENSQKTCIRIGTKPKSDCTPTVTVEVSSGQNGDE 356
QY 284 SVALHQRHVELL-----PARLAKSLALLGVFANCMAPSLFTIVLSFYSYA 332
DB 357 KONIVAKIVTKQAPAKKPPSEKKTITLAILLAFITMAPYVNMVLINTFCAPC 416
QY 333 TGPKSVWTRIAFMLOMNSFVNPPLYPCHKRFKQAF 369
DB 417 I-PMTVM-TIGVWLCYINSTINPACYALCNATFKRTF 451

RESULT 9

US-10-521-162-40
Sequence 40, Application US/10521162
Publication No. US20050287529A1
GENERAL INFORMATION:
APPLICANT: Brandt, Kevin S.
TITLE OF INVENTION: FLEA AND TICK OCTOPAMINE RECEPTOR NUCLEIC ACID MOLECULES,
FILE REFERENCE: FC-11-PCT
CURRENT APPLICATION NUMBER: US/10/521,162
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: 60/319,402
PRIOR FILING DATE: 2003-07-17
PRIOR APPLICATION NUMBER: 60/426,601
PRIOR FILING DATE: 2003-11-15
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PatentIn version 3.2
SEQ ID NO 40
LENGTH: 480
TYPE: PRT
ORGANISM: Rhipicephalus sanguineus
US-10-521-162-40

Query Match 19.0%; Score 384.5; DB 6; Length 480;
Best Local Similarity 25.9%; Pred. No. 1.2e-26;
Matches 115; Conservative 67; Mismatches 161; Indels 101; Gaps 13;

QY 16 VTLAFPMGLVAFNMLGNALVLAFAVVDKNLRHRSYFELNLAISDFVGVISFLYTPH 75
DB 20 VALFFVGLSINGLVIFGNLVLIVIAVLAFTKLTNTVNFVSLAVADLSVGLTVLPSYIVL 79
QY 76 TLFE-WDGGKEICVMTLDYLLCTASVYNYLISYDRILSYSNVSVRTQHTGVKIVT 134

DB 80 EVLEWIFGHTWCQIWLAVDMLCTSSILNLCAISVDRYLAITRPVRSIMSS--RRAKL 138
QY 135 LMVAVWVLAFLVNGPMILVSSWKDESE-----CEPG-- 167
DB 139 LIVAVWVLAFLVNGPMILVSSWKDESE-----CEPG-- 167
QY 168 --FSEWYIILATSFLEFVPIVLAFAFMNNTYWSLMK--RDHLSCQSHPGGLTAVSNICGHSF 228
DB 196 VLINNGKVI-YSLGSGYIIPMLFMFPNNRYIAAIAQTGRALBRGPIITTSKIKGRRT 254
QY 201 --LMKDH-----LSRCQSHPGGLTAVSNICGHSFPGGLSRRSLAST----- 242
DB 255 DQRLTLVRHGRNDSANNAKRGSEHLAGETCIDGIVTGRRRPGLKSRDEPSASRSASK 314
QY 243 -----EVASFSEQRKRS-LMSSRTKMN---SNTIASKGSGFSQS--D 283
DB 315 TROQSDORTTSAPSPFSKNSGARS-----GRNTSTSGGCKGSRSSKRSQKW 365
QY 292 HVELLRAR-RLAKSLAILLGVFANCMAPSLFTIVLSFYSATGPKSVWTRIAFMLOMNSF 350
DB 366 QAKRFTBAKTKVGTIVGFCICMLPFTVYIVRAFCHECT--PNLLFSGVFTMLGYCN 423
QY 351 SFVNPPLYPCHKRFKQAFKIFC 374
DB 424 SAINPLIVLVSKDFRLAFKRLC 447

RESULT 10

US-11-127-877-51
Sequence 51, Application US/1127877
Publication No. US20050287565A1
GENERAL INFORMATION:
APPLICANT: Merchiers, Pascal G.
APPLICANT: Hoffmann, Marcel
APPLICANT: Spittela, Koentraad F. F.
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
FILE REFERENCE: P27, 800-B USA
CURRENT APPLICATION NUMBER: US/11/127,877
CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: 60/570,352
PRIOR FILING DATE: 2004-05-12
PRIOR APPLICATION NUMBER: 60/603,948
PRIOR FILING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 590
SOFTWARE: PatentIn version 3.3
SEQ ID NO 51
LENGTH: 429
TYPE: PRT
ORGANISM: Homo sapiens
US-11-127-877-51

Query Match 18.7%; Score 377.5; DB 7; Length 429;
Best Local Similarity 27.6%; Pred. No. 4.6e-26;
Matches 110; Conservative 73; Mismatches 129; Indels 87; Gaps 20;

QY 10 LSLSTVTLAFEM-SLVAFAIMGNALVLAFAVVDKNLRHRSYFELNLAISDFVGVIS 68
DB 21 VNISKAILGLVILGLILFGV-LGNILVILSVACHRHLSVTHRYIVLAVADLLITSTV 79
QY 69 IPLYIHTLPF---WDFGKEICFVMTLDYLLCTASVYNYLISYDRILSYSNVSVNYSR- 123
DB 80 LFP---SAIFPVGLVGMVGRVFCINMAVDVLCCTASIMGCTISIDRYIVSVSPRYPT 136
QY 124 --TQHTGVKIVTLNVAVWVLAFAVVDKNLRHRSYFELNLAISDFVGVISFLYTPH 172
DB 137 IVTQRRGLM---ALLCYMNLISVIGPLF---GRQAPABEDETICQINEEG----- 183
QY 173 YIL--AITSFLEFVPIVLAFAFMNNTYWSLMKRDHLSCQSHPGGLTAVSNICGHSF 230
DB 184 YVLSALGSFY-LPLAILLVVYCRVYV-----VAKRBSRG 217

QY 231 RLSS-RSLSSSTEVPAFSEHSEORRKSLSMFSSRTKNSNTIASKMGFSQSDVALHQ 289
 Db 218 LKSGIKTDKSDSEQVTLIRHRKNAPAGSGMASAKTKHF-----SVRL-- 261
 QY 290 REHELLARBARLAKSLAILLGVFAVCMA PYSLEFTIVLSFYSSATGPKSVWYRIAFWLQMF 349
 Db 262 ---LKFSREKKAQKTLGIVGCFVLCMLPFLVMPIGSFPPDFK-PSETVKIYVWLGYL 317
 QY 350 NSFVNPPLIYPLCHKRFQKAF---LKIPIKQPLPSQHS 385
 Db 318 NSCINPIIYPCSSQGEFKKAFQVNLRIQCLRRKQ--SSKHA 355

RESULT 11

US-11-127-877-50
 ; Sequence 50, Application US/11127877
 ; Publication No. US20050287565A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Merchiers, Pascal G.
 ; APPLICANT: Hoffmann, Marcel
 ; APPLICANT: Spittels, Koenraad F. F.
 ; APPLICANT: Laenen, Wendy
 ; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
 ; TITLE OF INVENTION: Amyloid-Beta Protein Production
 ; FILE REFERENCE: P27,800-B USA
 ; CURRENT APPLICATION NUMBER: US/11/127,877
 ; CURRENT FILING DATE: 2005-05-12
 ; PRIOR APPLICATION NUMBER: 60/570,352
 ; PRIOR FILING DATE: 2004-05-12
 ; PRIOR APPLICATION NUMBER: 60/603,948
 ; PRIOR FILING DATE: 2004-08-24
 ; NUMBER OF SEQ ID NOS: 590
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 50
 ; LENGTH: 466
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-127-877-50

Query Match 18.7%; Score 377.5; DB 7; Length 466;
 Best Local Similarity 27.6%; Pred. No. 5e-26;

Matches 110; Conservative 73; Mismatches 129; Indels 87; Gaps 20;

QY 10 LSLSTRVTLAEFM-SLVAFAIMLGNALVILAEVVDKRLRHSRYFLNLAIISDFEYVIS 68
 Db 21 VNISKAILLGVILGLILFGV-LGNILVILSVACHRHLSVTHYIYVNLAVADLLTSTV 79
 QY 69 IPIYIPIHLE---WDFGEKICVFWLTTDYILCTASVYNYVLISYDRYLSVSNVSR- 123
 Db 80 LPIF---SAIFELGYMAFGRAFCNMAVDVLCCTASIMGLCTISIDRYIGVSPRLRYPT 136
 QY 124 --TOHTGVAKITVTLVAVVAVLAVLN-GPMILVSESMDEGSE---C---EPGFSEW 172
 Db 137 IVTQGRGLM---ALLCVWALSIVISIGPLF---GMQPAPEDDITIOINBERP----- 183
 QY 173 YIL-AITSFLEFVIVPILVAFNNIYWSLWKRDLHSRCSHGELTAVSSNICHSFRG 230
 Db 184 YVLSALGSFY-LPLAILLWVCRYV-----VAARBSRG 217
 QY 231 RLSS-RRLSSASTVPAFSEHSEORRKSLSMFSSRTKNSNTIASKMGFSQSDVALHQ 289
 Db 218 LKSGIKTDKSDSEQVTLIRHRKNAPAGSGMASAKTKHF-----SVRL-- 261
 QY 290 REHELLARBARLAKSLAILLGVFAVCMA PYSLEFTIVLSFYSSATGPKSVWYRIAFWLQMF 349
 Db 262 ---LKFSREKKAQKTLGIVGCFVLCMLPFLVMPIGSFPPDFK-PSETVKIYVWLGYL 317
 QY 350 NSFVNPPLIYPLCHKRFQKAF---LKIPIKQPLPSQHS 385
 Db 318 NSCINPIIYPCSSQGEFKKAFQVNLRIQCLRRKQ--SSKHA 355

RESULT 12

US-10-875-716-10
 ; Sequence 10, Application US/10875716
 ; Publication No. US20050266522A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Li et al.
 ; TITLE OF INVENTION: Human Amine Receptor
 ; FILE REFERENCE: P1186D1C2
 ; CURRENT APPLICATION NUMBER: US/10/875,716
 ; CURRENT FILING DATE: 2004-06-25
 ; PRIOR APPLICATION NUMBER: US 09/988,745
 ; PRIOR FILING DATE: 2001-11-20
 ; PRIOR APPLICATION NUMBER: US 09/314,006
 ; PRIOR FILING DATE: 1999-05-19
 ; PRIOR APPLICATION NUMBER: US 08/467,559
 ; PRIOR FILING DATE: 1995-06-06
 ; NUMBER OF SEQ ID NOS: 10
 ; SEQ ID NO 10
 ; LENGTH: 353
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-875-716-10

Query Match 18.5%; Score 375; DB 6; Length 353;
 Best Local Similarity 26.4%; Pred. No. 6.1e-26;
 Matches 97; Conservative 79; Mismatches 135; Indels 56; Gaps 10;

QY 19 AFMSLVAFAIMLGNALVILAEVVDKRLRHSRYFLNLAIISDFEYVISIP--LYIPIHT 76
 Db 29 ATLLTLIAIVVFGNAVLCMAVSREKALQTTNLYILSVLAVADLLVATLVMPWVYTL-EV 87
 QY 77 LFENDPKKEICVFELTLDYILCTASVYNYVLISYDRYLSVSNVSRHOGVAKITVLM 136
 Db 88 VGEWKFSEIRHCDIVTLDVWMCCTASIMLNLCAISIDRTTAAMPMLINTRYSKRYVTMI 147
 QY 137 VAVVAVLAFVNGPML-VSESMKDEGSECEPGEFSEWYIATISFLEFVIVPILVAVFNM 195
 Db 148 SIWVLSFTISCPILPGLNADQNECIANPAF-----VYSSIVSPVYFVITLVYI 201
 QY 196 NIYWSLWKRDLHSRCSHGELTAVSSNICHSFGRLSRRS---LSASTVPAFSEH 252
 Db 202 KIYVILRR-----RKRYVTYKSSRAFAHLAPLKEAAR 237
 QY 253 QRR-----KSLMESRTKNSNTIASKMGFSQSDVALHOREHELLARBARLAKSL 305
 Db 238 EKGNHARDHPRIAKIFEIQTMPNGKT-----RTSLTKMSRRKLSQKKEKATOML 287
 QY 306 AILGVFAVCMA PYSLEFTIVLSFYSSATGPKSVWYRIAFWLQMFNSFVNPPLIYPLCHKRF 365
 Db 288 AIVGVFIICMLPF-FITHLINHDCNIP-PVLYSAFTWLGYNASVNPPIITTFNIEF 345
 QY 366 QKAFLEKI 372
 Db 346 RKAFLEKI 352

RESULT 13

US-11-249-847-582
 ; Sequence 582, Application US/11249847
 ; Publication No. US20060035270A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lee, Frank D.
 ; APPLICANT: Meng, Dr. Xun
 ; APPLICANT: Chan, John W.
 ; APPLICANT: Zhang, Shengheng J.
 ; TITLE OF INVENTION: UNICORE RECOGNITION SEQUENCES AND METHODS OF USE THEREOF IN
 ; TITLE OF INVENTION: PROTEIN ANALYSIS
 ; FILE REFERENCE: EP7M-P05-001
 ; CURRENT APPLICATION NUMBER: US/11/249,847
 ; CURRENT FILING DATE: 2005-10-12
 ; PRIOR APPLICATION NUMBER: 10/436,549
 ; PRIOR FILING DATE: 2003-05-12
 ; PRIOR APPLICATION NUMBER: 60/379,626

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; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/393,137
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/393,197
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/393,211
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/393,223
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/393,233
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/393,235
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/393,280
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/430,948
; PRIOR FILING DATE: 2002-12-04
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 614
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 582
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-249-847-582

Query Match      18.4%; Score 372; DB 7; Length 487;
Best Local Similarity 23.0%; Pred. No. 1.6e-25;
Matches 107; Conservative 85; Mismatches 159; Indels 114; Gaps 14;

QY 18 LAFFNSVAFAMIGNALVILAFVVDKXLRHRSYFFLALISDFVGVISIPVILPHL 77
DB 30 LVVVTSTICLVTVGNLVLVAVRSERKLTWGNLTVLSVADLVGVAVPMNLYL 89
QY 78 F-EMDFGKEICVFWLTTDYLTCTASVYVILISYDRYLSVSNVSVRYGHTGVKLITLM 136
DB 90 MSKMLGRPLCLFMSMDVASTAFISFVILCIDRYSVOQPLRLKRTTRASATLL 149
QY 137 VAVWVLAFLVNGPMI---LVSESWKDEGSECEPGFSEWYILATISFLEPIVILVAV 192
DB 150 GA-WFLSFLMWPIILGMNHFMOOTSVRREDKCTDPDYVTFPKWTAIINFYLPILMLM 208
QY 193 FNNMIVNMLMRDHSRCQ-----SHPGLTAVS---SNIGHSR-GR----- 231
DB 209 FYAKIYKAV--RQH---CQRELINRSLPFSFSEIKLRPNPKGDAXKPKKSPMEVLRK 263
QY 232 -----LSSRRSLASTEVPAFHSERQRKKSILMF-----SSR----- 264
DB 264 PKDAGGSVLKSPSQTPKEMKSPVVFSSQDDREVDKLYCFPLDIYHMOALAGSSRDYVA 323
QY 265 -----TTONSNTJASKMSFSQSOSDS----- 284
DB 324 VNRSHGLKTDEQGNTHGASEISSEDMQMGDSQSFRTSDTTTJAPCKGLRGSNTG 383
QY 285 -----VALHREHVELL---RARRLAKSLAILLGVFVAVCAPSLFTIVLSPSS 331
DB 384 LDYIKFTWKRILSHSRROYSGIHMNRERKAKOLFIMAAFLICWIPYFIFFMVIAFCN 443
QY 332 ATGPKSVWYRIAFWLOWENSPVNPPLLYPLCHKRPQKAFKICIK 376
DB 444 CNEHLHMFPTI--WIGYINSTINPLIYPLCNEHFKTKRILHIR 486

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RESULT 14
US-10-499-210-2
Sequence 2, Application US/10499210
Publication No. US20060052435A1

GENERAL INFORMATION:
APPLICANT: Pfizer Limited and Pfizer, Inc.
TITLE OF INVENTION: Compounds for the Treatment of Sexual
FILE REFERENCE: PC22046A
CURRENT APPLICATION NUMBER: US/10/499,210

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; CURRENT FILING DATE: 2004-06-14
; PRIOR APPLICATION NUMBER: GB 0130219.9
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-499-210-2

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Query Match 17.2%; Score 348.5; DB 6; Length 400;
Best Local Similarity 28.9%; Pred. No. 1.6e-23;
Matches 111; Conservative 66; Mismatches 140; Indels 67; Gaps 14;

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QY 28 AIMGNALVILAFVVDKXLRHRSYFFLALISDFVGVISIP--LYIPHLFEMDFGKE 85
DB 42 AIVFNGLVCAVLERALQTTNYLVVSLAVADLVAVLWPMVYVLEVTVGVNMFRI 101
QY 86 ICFWLTDDYLTCTASVYVILISYDRYLSVSNVSVR--TQHTGVAKIVTLMAVWYLA 143
DB 102 CCDVFVTLVVMWCTASILNLCAISIDRYTAVMPVHYGTOSSCRVVALMTAVWYLA 161
QY 144 FLVNGPMILVSESWKDEG--SECEPGFSEWYILATISFLEPIVILVAVPMNLYSL 201
DB 162 FAVSCPLLFGFRITGDDPVTVCISINDFVI--YSSVSYFLPFGVTVLYVA-----RIYVYL 215
QY 202 WKRDHL-----SRCQS--HPGLTAVSSNIGHSEFGLSSRRSLASTEVPAFHSER- 252
DB 216 KQRRKRLITRQNSQCNVVRPGF-----PQQLSPD---PAHLELKRKY 255
QY 253 -----QRRSSLMFSRTKCN--SNTJASKM-----GSPQSOSVALH 288
DB 256 YSICQDTRALGGPGFQERGELKREKTNSSLPITAPLSLEVRKLSNGRSTSLKGLPL 315
QY 289 QREHVELRARRLAKSLAILLGVFVAVCAPSLFTIVLSPSSATGPKSVWYRIAFWLOW 348
DB 316 QPQGVF-LREKAYQMAIVIGAFIVCLPFFFL--THVANTHCQTCVSPBELYSATTWLCY 373
QY 349 FNSFVNPPLLYPLCHKRPQKAFIKI 372
DB 374 VNSALNPFVITYTTFNIEFRKAFIKI 397

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RESULT 15
US-11-165-024-3
Sequence 3, Application US/11165024
Publication No. US20050266527A1

GENERAL INFORMATION:
APPLICANT: Li et al.
TITLE OF INVENTION: Human G-Protein Receptor HIBEF51
FILE REFERENCE: PFI87D1C2
CURRENT APPLICATION NUMBER: US/11/165,024
CURRENT FILING DATE: 2005-06-24
PRIOR APPLICATION NUMBER: US 10/006,394
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 09/228,420
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: US 08/465,971
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.3
SEQ ID NO 3
LENGTH: 350
TYPE: PRT
ORGANISM: Homo sapiens
US-11-165-024-3

Query Match 17.0%; Score 344; DB 7; Length 350;
Best Local Similarity 26.5%; Pred. No. 3.5e-23;
Matches 99; Conservative 74; Mismatches 131; Indels 70; Gaps 14;

QY 11 SLSTRVTLAFPMISLVAFAMIGNALVILAFVVDKXLRHRSYFFLALISDFVGVISIP 70

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Db      29  SLQVTLTVCLAGLMLTVFGENVLITAVFTSRALKAPQNLFLVSLASADILVATLVIP 88
Qy      71  LYIPHTLF-EMDFGKEICVFWLTDTDYLLCTASVNIIVLISYDRYLSVSNVSYRTQHTGV 129
Db      89  FSLANEWGWYFGKAWCEIYLALDVLFTCTSIIVHLCAISLDRWYSITQAIENLKRTP 147
Qy     130  LKIYTLMAVAVYLAFLVNGPMILVSESWKDSGECEPC-----FSEWYILATISFLEF 183
Db     148  RRIKAIITVWVISAVISFPP-LISIEKKGGGQPPAPRCEINDOKWYVIS-SCIGSF 205
Qy     184  VIPVLIVAFNNNIYMSLMKRDHLSRCQSHPGLTAVSSNICGHSFRGLSSRRSLASTE 243
Db     206  PAPCLIMILVYRITQIAKRTVP--PSRRGPDVAAPPGLOGRGR-----SASG 255
Qy     244  VPASFSESRORRKSILMFSRTKNSNTIASKMGSFQSDSVALHQREHVELLRARLAK 303
Db     256  LP-----RRRA-----GAGGN-----REKRFTF 274
Qy     304  SLAILGVFAVCWADYSLEFIVLSFYSSATG--PKSVYRIAFWLMQENSFVNPPLYPL 360
Db     275  VLAIVIGVFVVCWPPF-FTYTL---TAVGCSVPRTL-FKPFVFWGYCNSLNPIYTI 328
Qy     361  CHKRQKAFKIFC 374
Db     329  FNHDFRAFKKILC 342
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Search completed: March 28, 2006, 14:03:32
Job time : 25 secs